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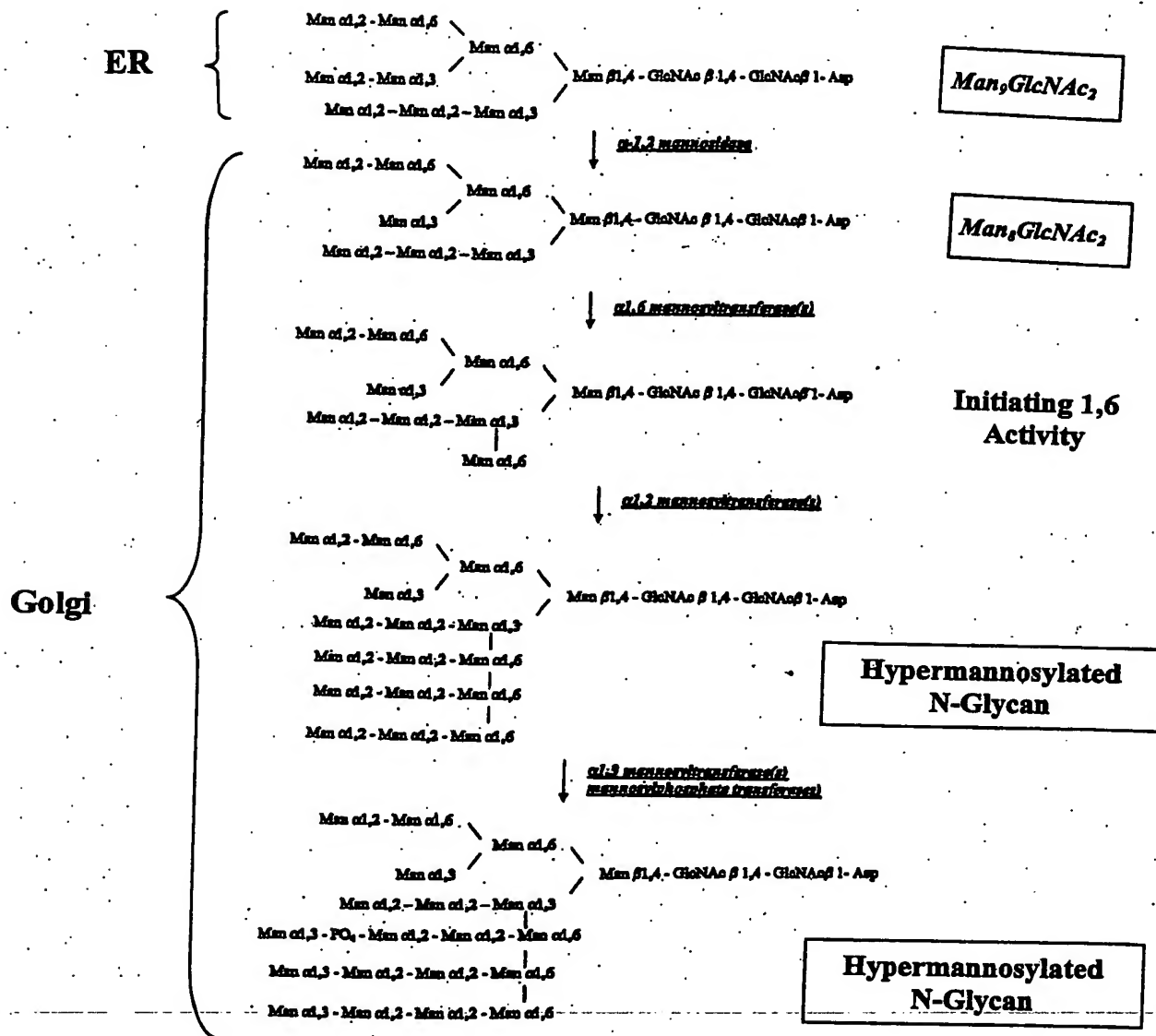


Fig. 1A



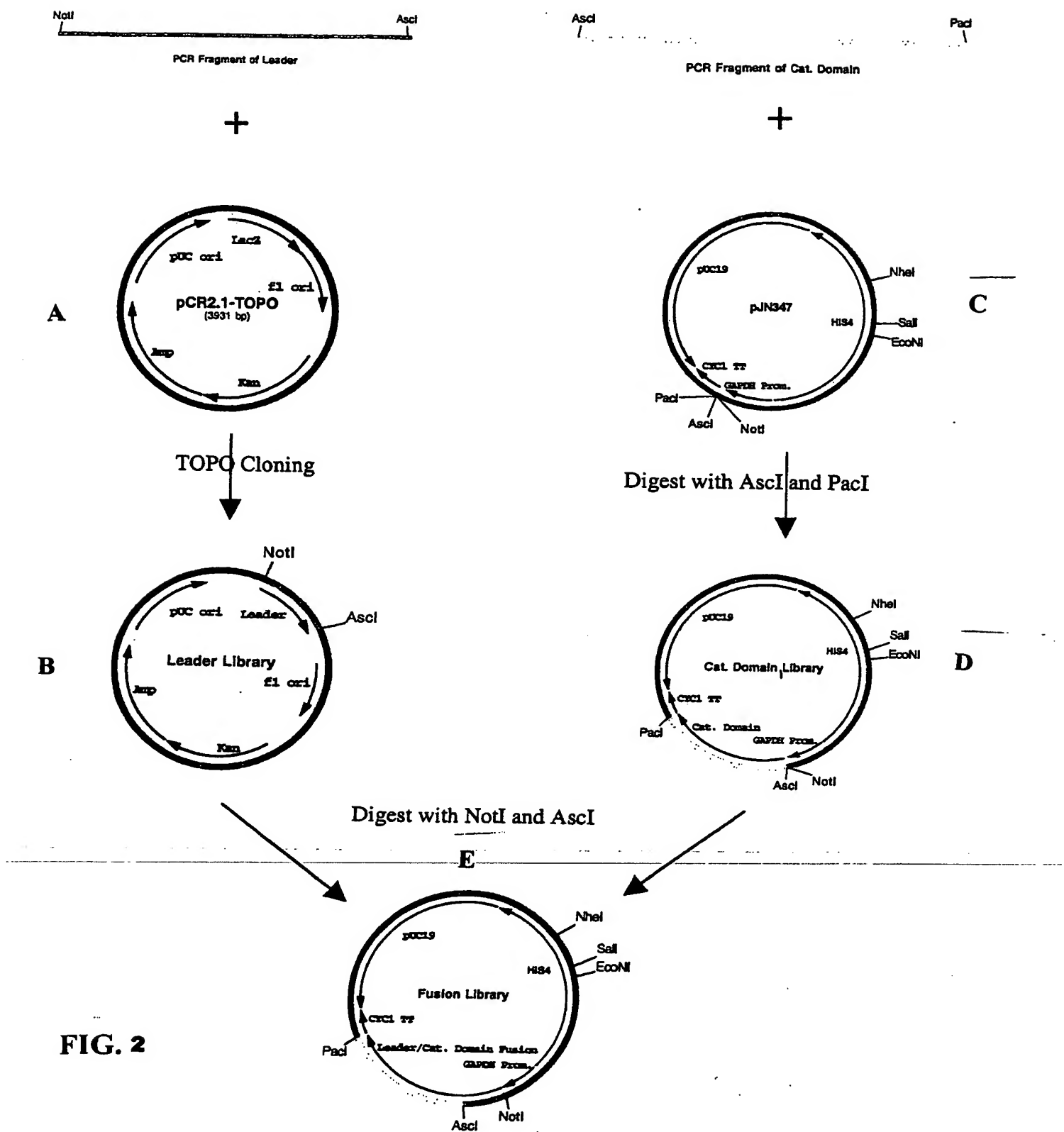
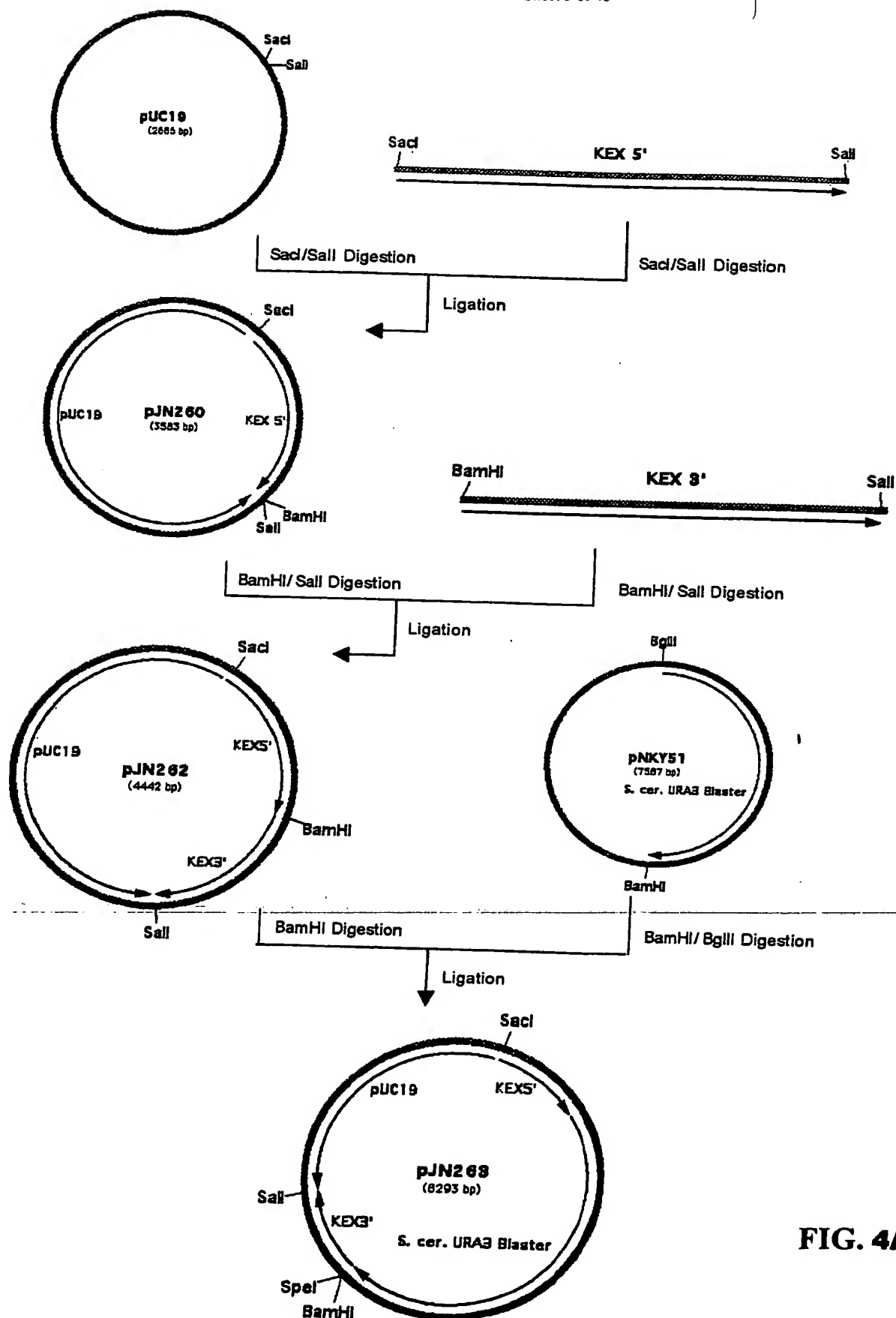


FIG. 2

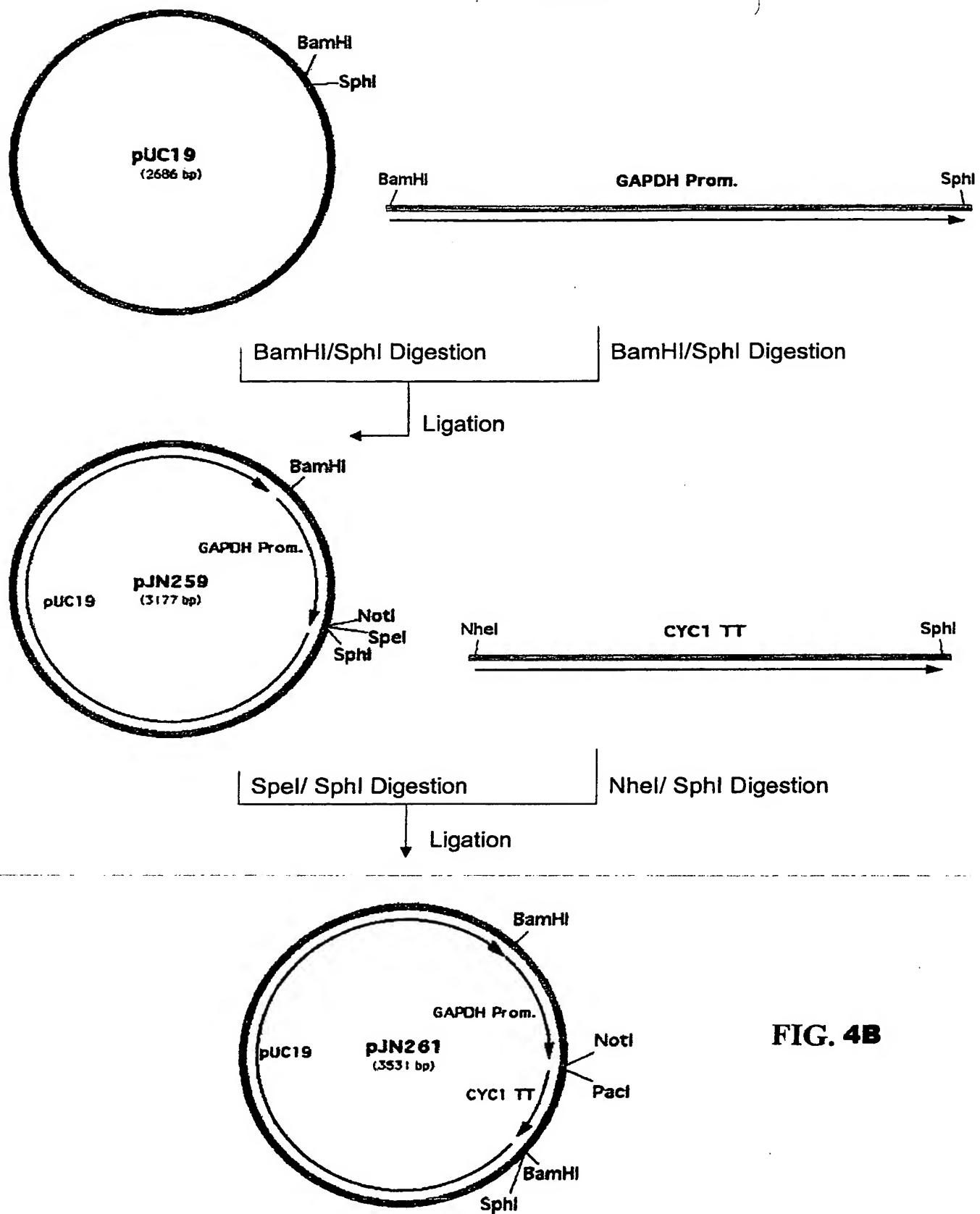
### FIG. 3

**M. musculus alpha-1,2-mannosidase IA open reading frame.** The transmembrane and catalytic domains are highlighted in bold respectively. The sequence of the primers used to generate the N-terminal truncations are highlighted by underlining and the start of each respective protein fragment indicated by an arrow.

```
1 atgcccgtgggggctgttgcgcctcttcagtagccctggggggcgccgctggcagtgccctgggcggggggcttggcgggcgaggagggg
1▶ M P V G G L L P L F S S P G G G G L G S G L G G G L G G G R K G
97 tctggccccgctgccttccgctccaccgagaagtctcgtgctgctgctggtgttcagcgcccttcacacgctctgcttggggcaatc
33▶ S G P A A F R L T E K F V L L L V F S A F I T L C F G A I
184 tcttctctgcttgaatctctccagctgctcagcggggtctggtccactcccaacctgcttgcagccgcccggcgagcacaagcccggtctg
62▶ F F L P D S S K L L S G V L F H S N P A L Q P P A E H K P G L
d65 primer
278 gggcgctgcggaggatgcgcgcgggggagagtcgggcccgcgagggagggcgccctgggggaccccgaggctgggactggaagacaacttagcca
93▶ G A R A E D A A E G R V R H R E E G A P G D P G A G L E D N L A
d105 primer
374 ggatccgcgaaaccacgagcggtctctcaggggaagccaaggagacctgcagaagctgcggaggagatccaaagagacattctgctggagaagg
125▶ R I R E N H E R A L R E A K E T L Q K L P E E I Q R D I L L E K
470 aaaaggtggcccgagaccagctgcgcgacaaggatctgttttaggggcttgcaccaagggtggacttctgcccccgctcggggtagagaaccgggagc
157▶ E K V A Q D Q L R D K D L F R G L P K V D F L P P V G V E N R E
d187 primer
566 ccgctgacgcaccatccgtggaagaggggcaagatcaaaagagatgatgacccatgcttggaaataattataaacgctatgcgtggggc
189▶ P A D A T I R E K R A K I K E M M T H A W N N Y K R Y A W G
655 ttgaacgaactgaacctatatcaaaagaaggccattcaagcagtttctgttggcaacatcaaaaggagctacaatagtagatg
219▶ L N E L K P I S K E G H S S S L F G N I K G A T I V D
737 ccttggatacccttttcttattatgggcatgaagactgaatttcaagaagctaaatcgtggattaaaaaatatttagatttttaa
246▶ A L D T L F I M G M K T E F Q E A K S W I K K Y L D F N
819 tctgaatgctgaagttctgttcttttgaagtcacacatagcttctgctgggactgctgtcagcctactatttgcggagag
273▶ V N A E V S V F E V N I R F V G G L L S A Y Y L S G E
901 gagatatttccgaagaagcagtggaacttgggggtaaaattgctacactgcatcttccatactccctctggaatcccttgggcat
301▶ E I F R K K A V E L G V K L L P A F H T P S G I P W A
983 tctgtaatatgaagaagtggtgacggcggaactggcccttgggctctggaggcagcagtatccctggccgaatttgggaactct
328▶ L L N M K S G I G R N W P W A S G G S S I L A E F G T L
1065 gcattttagagtttatgcacttgtcccacttatcaggagagaccagctcttgcggaaaaggttatgaaattccgaacagtggtg
355▶ H L E F M H L S H L S G D P V F A E K V M K I R T V L
1147 acaaaactggacaaaaccagaaggcctttatcctaactatctgaaccccgtagtgagacagtggtgggtcaacatcatgtgtcgg
383▶ N K L D K P E G L Y P N Y L N P S S G Q W G Q H H V S
1229 tgggaggacttgggagacagcttttatgaatatttgccttaaggcggtggtcaatgtctgacaagacagatctcgaagcgaagaa
410▶ V G G L G D S F Y E Y L L K A W L M S D K T D L E A K K
1311 gatgtatttggatgctgttcaggccatcgagactcacttgatccgcaagtcgaagtggggactaacgtacatcgcagagtg
437▶ M Y F D A V Q A I E T H L I R K S S G G L T Y I A E W
1393 aaggggggctcctctggaaacacaaagatgggcccactgacgtgcttgcaggaggcatgtttgcacttggggcagatggagctc
465▶ K G G L L E H K M G H L T C F A G G M F A L G A D G A
1475 cggaaagcccgggcccaactaacttgaactcggagctgaatttgcggcacttgcataatcttataatcgtacatatgt
492▶ P E A R A Q H Y L E L G A E I A R T C H E S Y N R T Y V
1557 gaagtgggaccgggaagcgttttcgatttgcgttgcgttgcggagctatttgcacagaggcaaatgaaaagtattacatctta
519▶ K L G P E A F R F D G G V E A I A T R Q N E K Y Y I L
1639 cggcccgaggtcatcgagacatacatgtacatgtgtgcgactgactcacgaccccaagtacaggacctgggctgggaagccg
547▶ R P E V I E T Y M Y M W R L T H D P K Y R T W A W E A
1721 tggaggctctagaaagtccactgcagagtgaaacggagggtactcaggcttaccgggatgtttacatttcccgctgagagttatga
574▶ V E A L E S H C R V N G G Y S G L R D V Y I A R E S Y D
1803 cgatgtccagcaagtttcttctggcagagacactgaagtatttgccttacttgatatttccgatgatgaccttcttccacta
601▶ D V Q Q S F F L A E T L K Y L L I F S D D D L L P L
1885 gaacactggatottcaaacacggaggtcctccttccctatactccgtgaacagaagaaaggaattgatggcaagagaaatga
629▶ E H W I F N T E A H P F P I L R E Q K K E I D G K E K
```



**FIG. 4A**



**FIG. 4B**

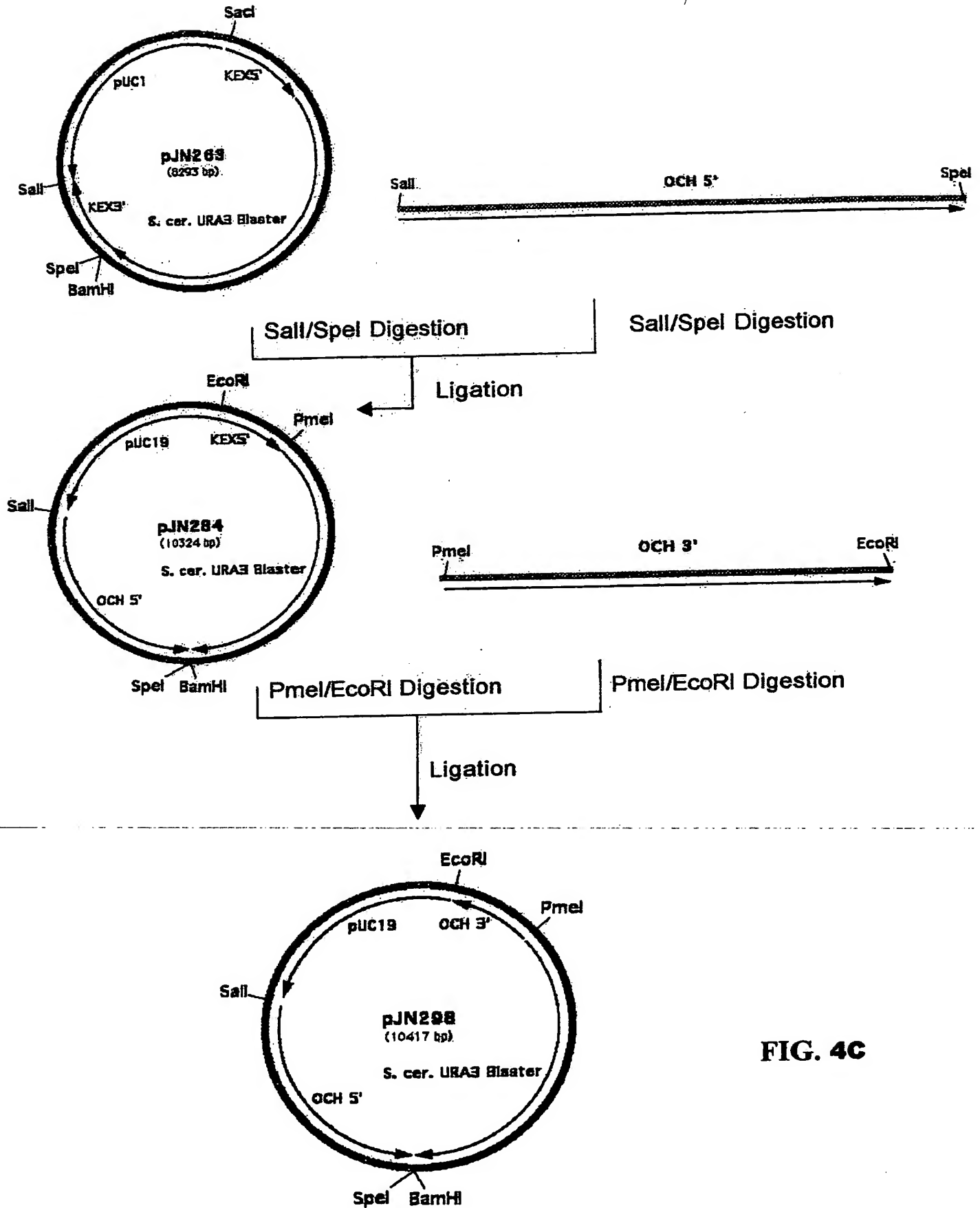
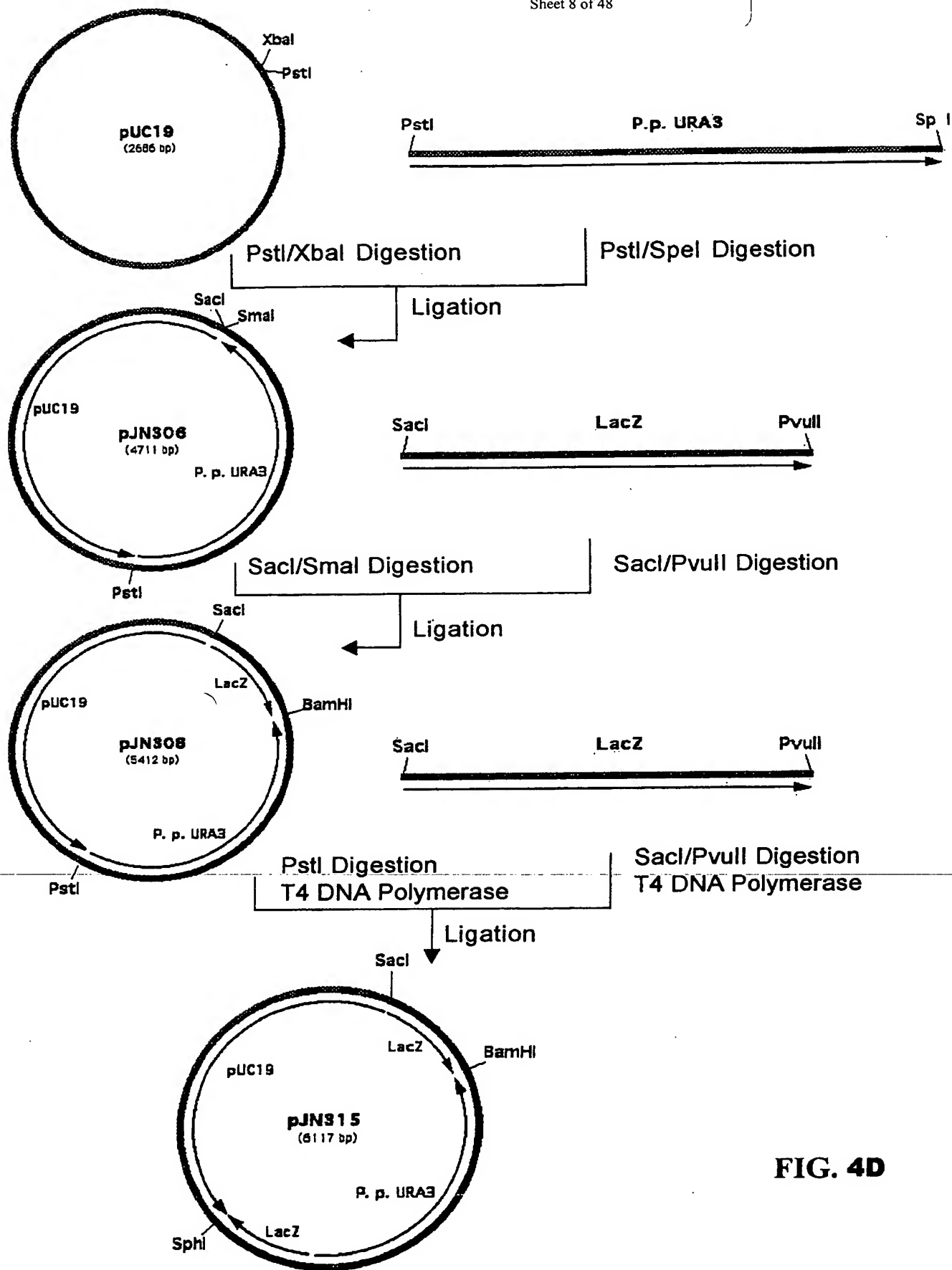


FIG. 4C





**FIG. 4D**

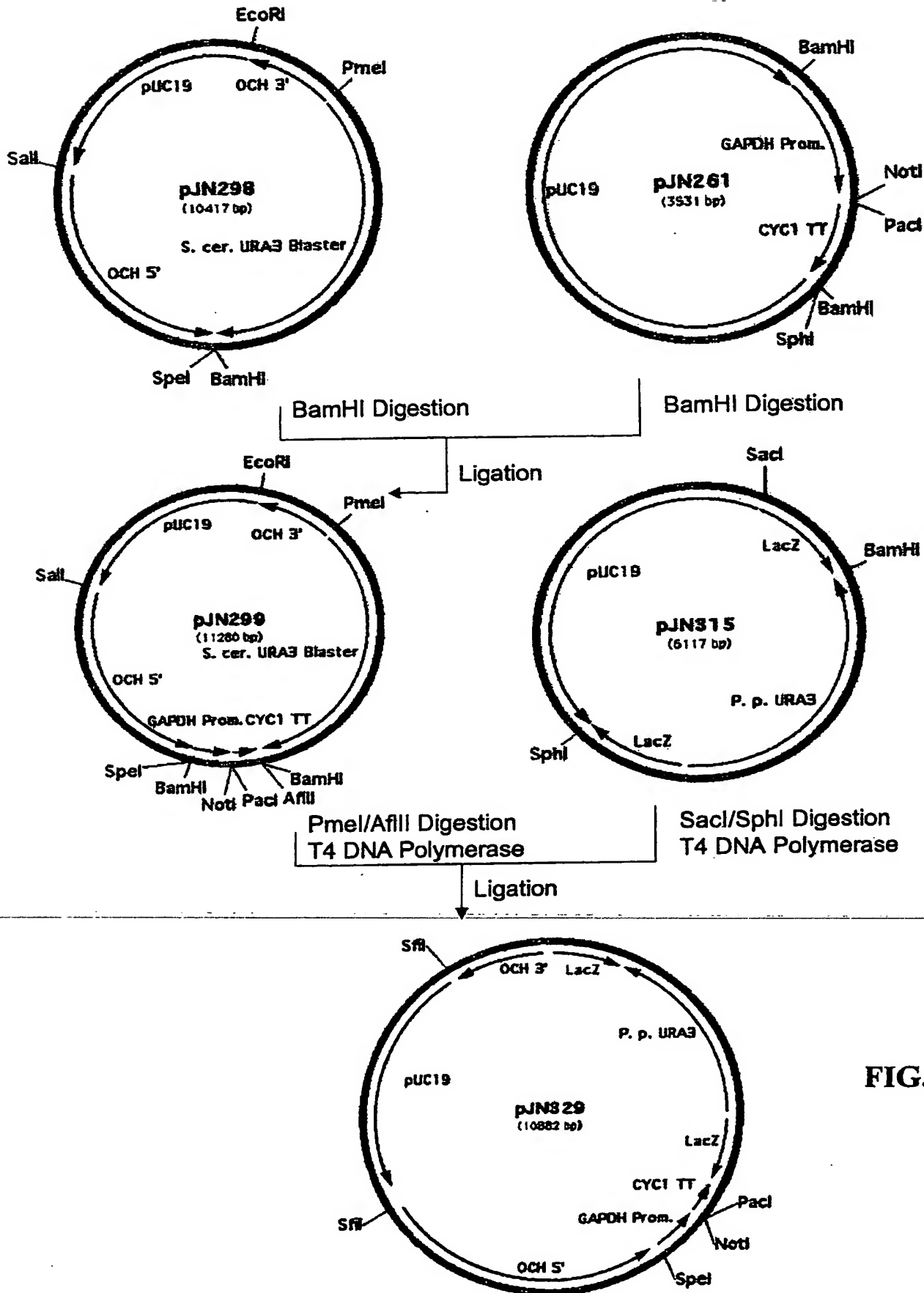
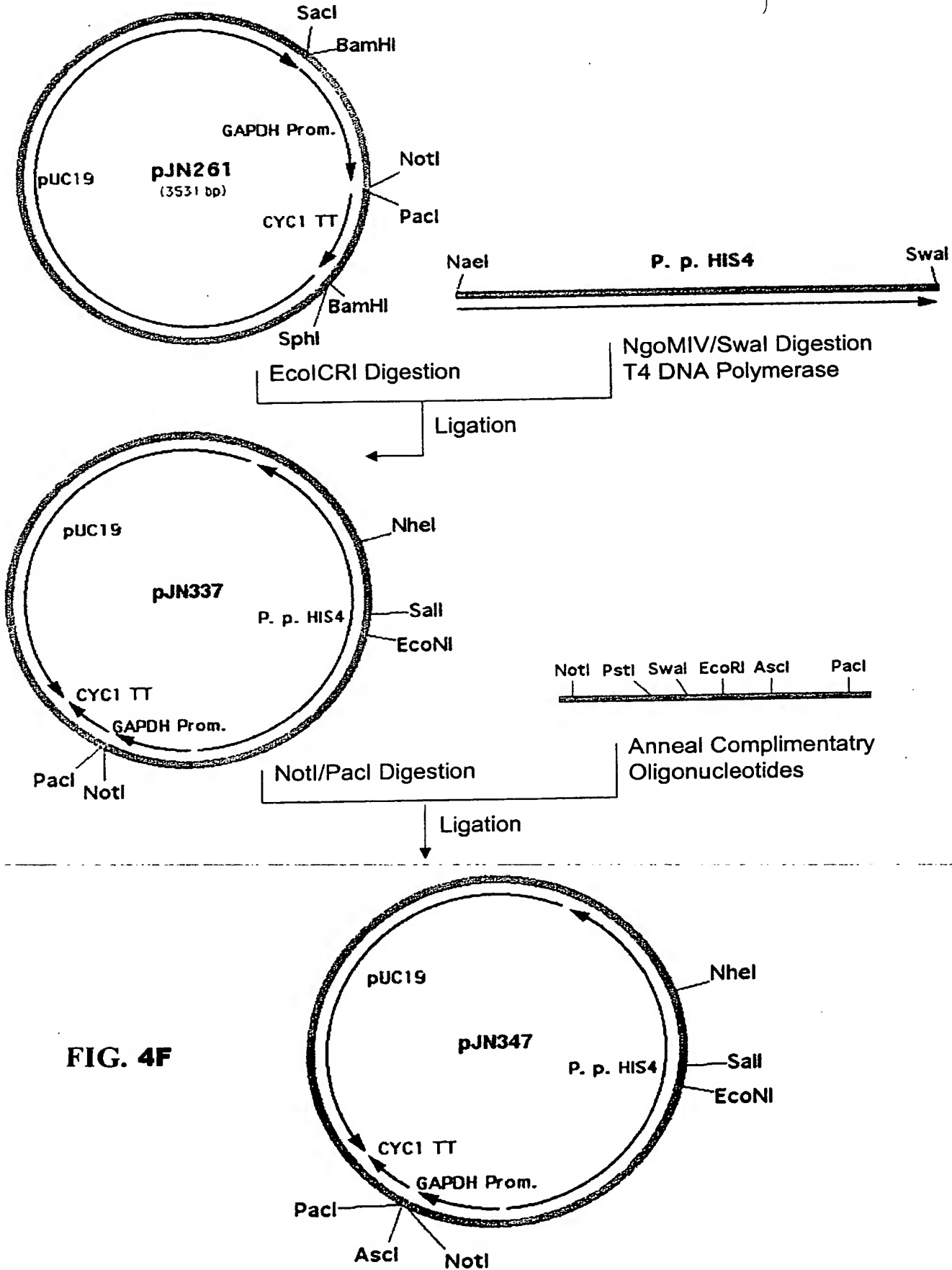
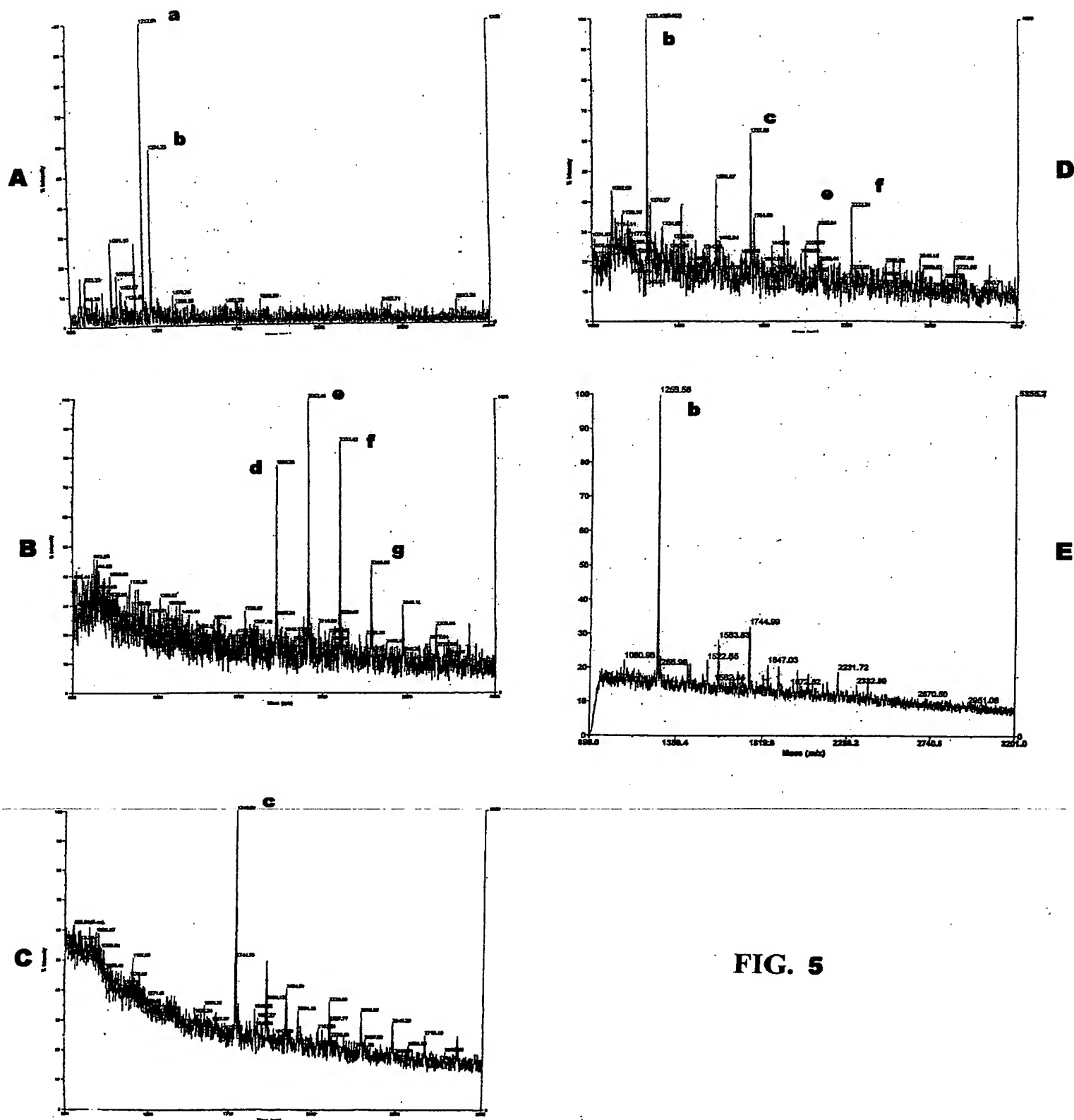


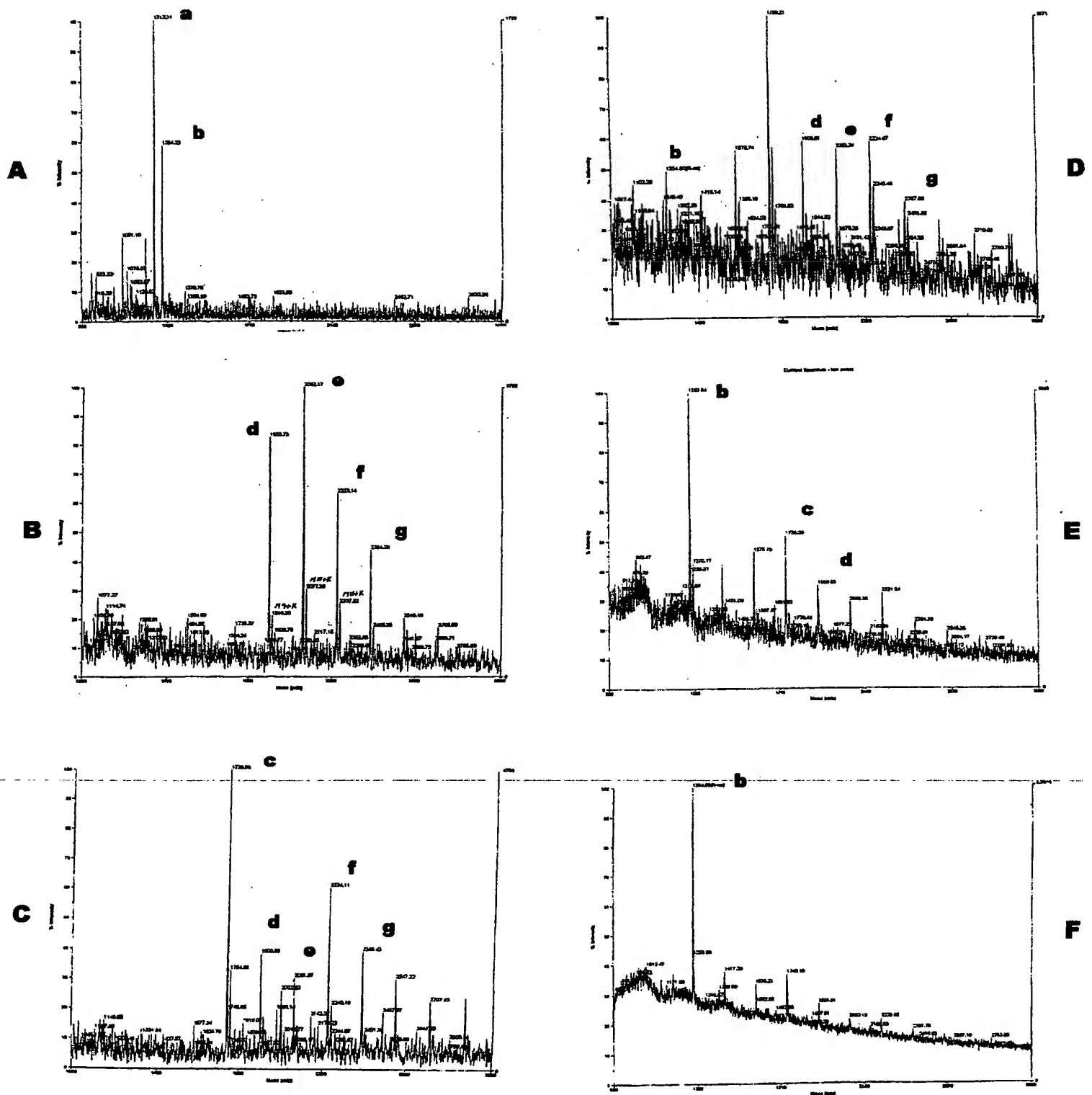
FIG. 4E



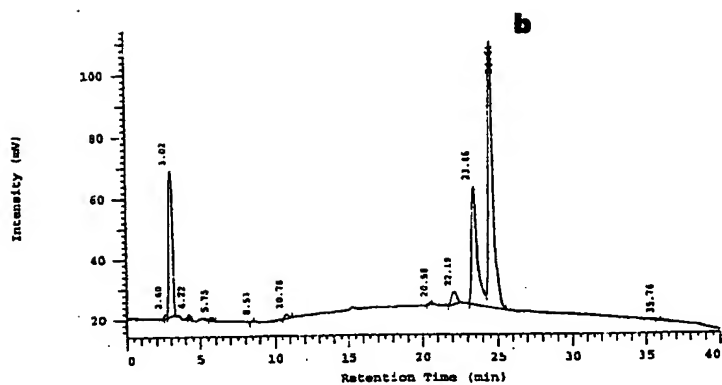
**FIG. 4F**



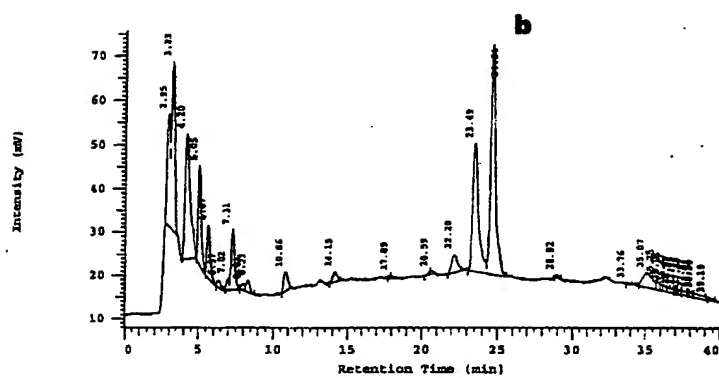
**FIG. 5**



A



B



C

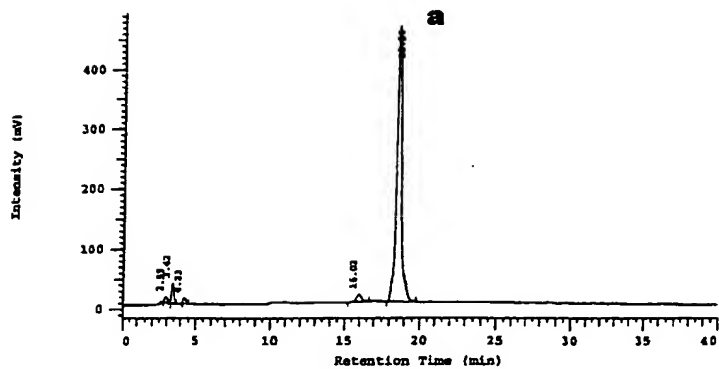
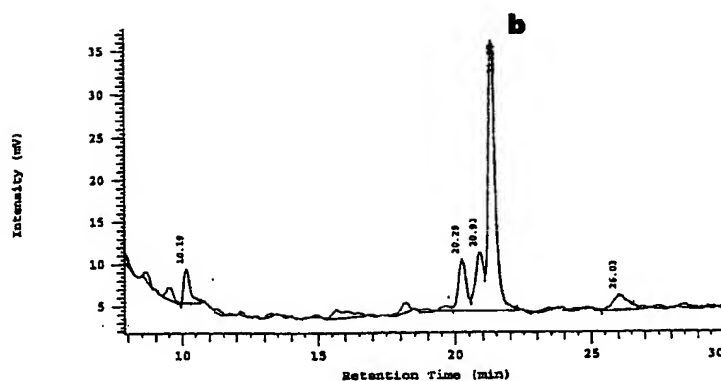
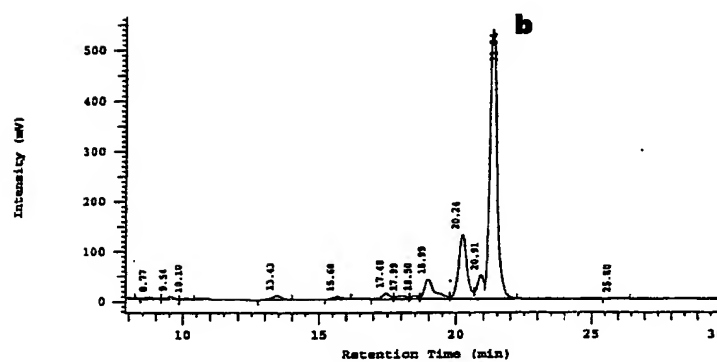


FIG. 7

A



B



C

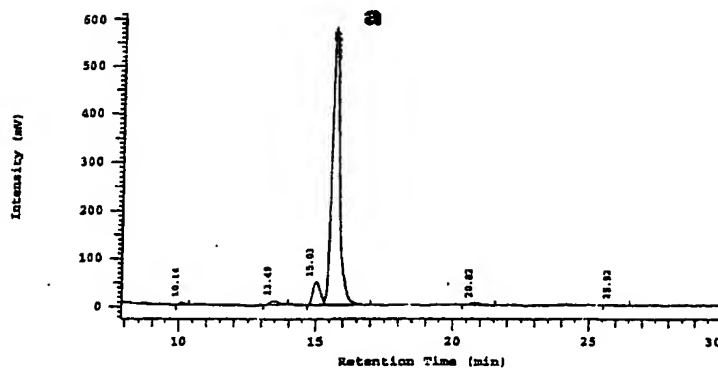
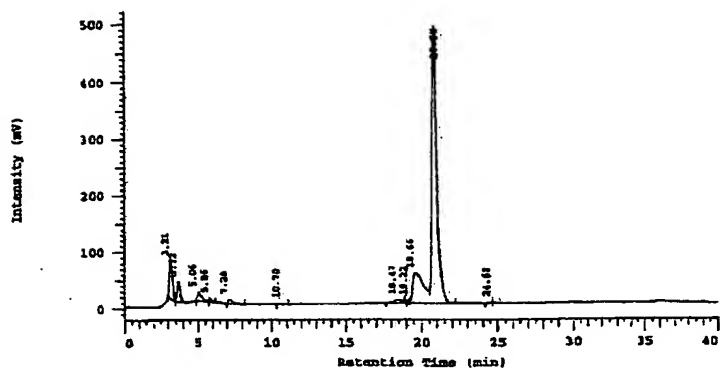
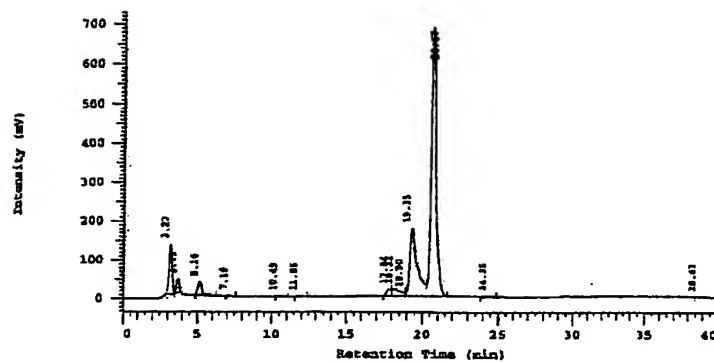


FIG. 8

A



B



C

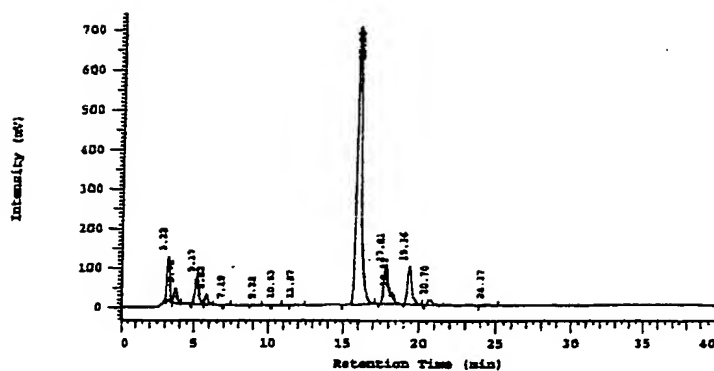
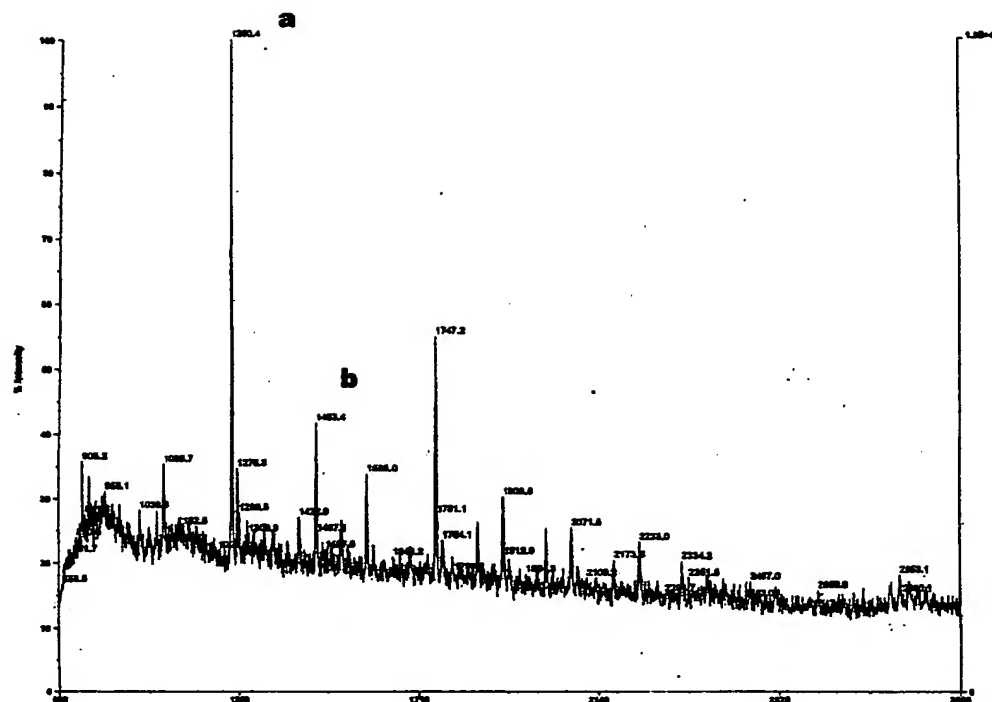


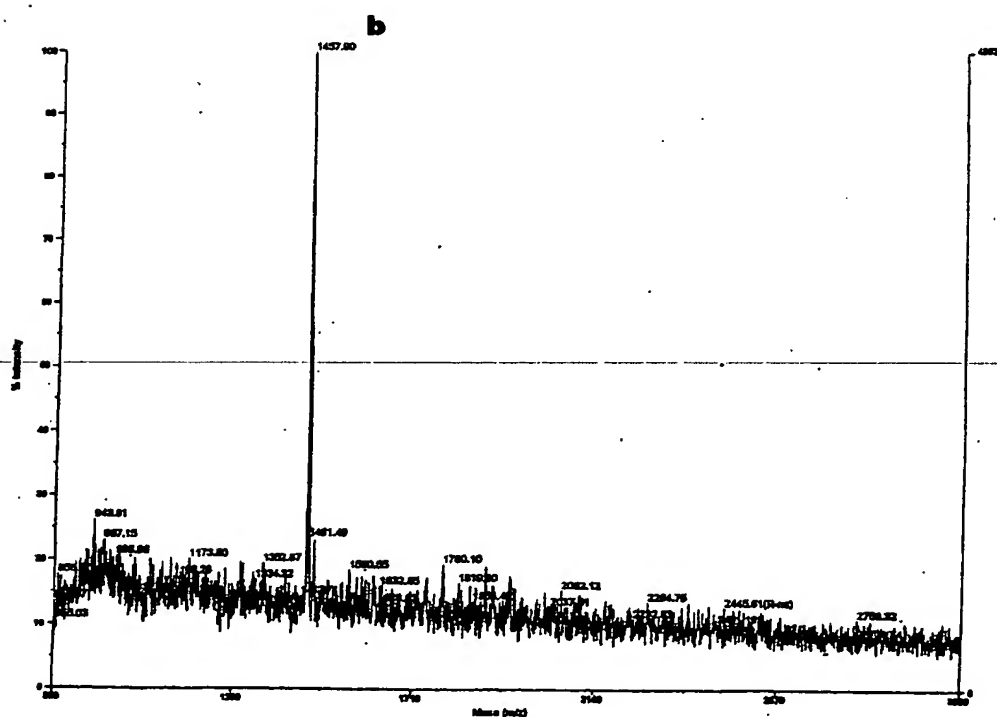
FIG. 9



**FIG. 10**



**A**



**B**

**pH optimum for BB27-2 medium**  
**C. elegans Mann1B D31 and S. Mnn10-s**

pH	% f Man5
4.5	0
5	32
5.5	41
6	35
6.43	22
6.5	4
7.5	0
8.5	0

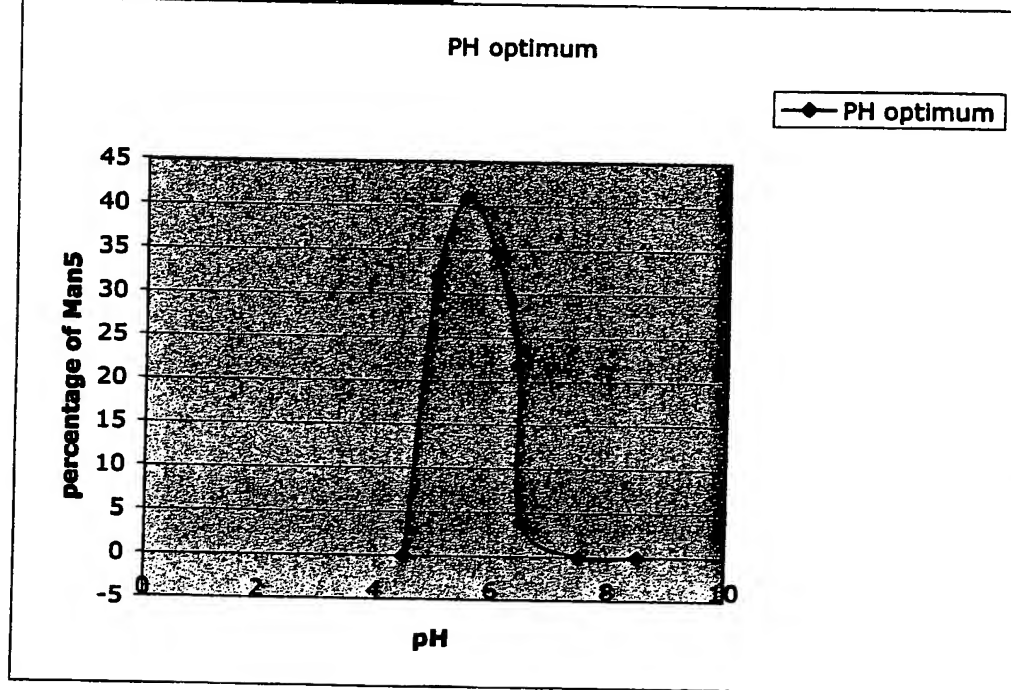
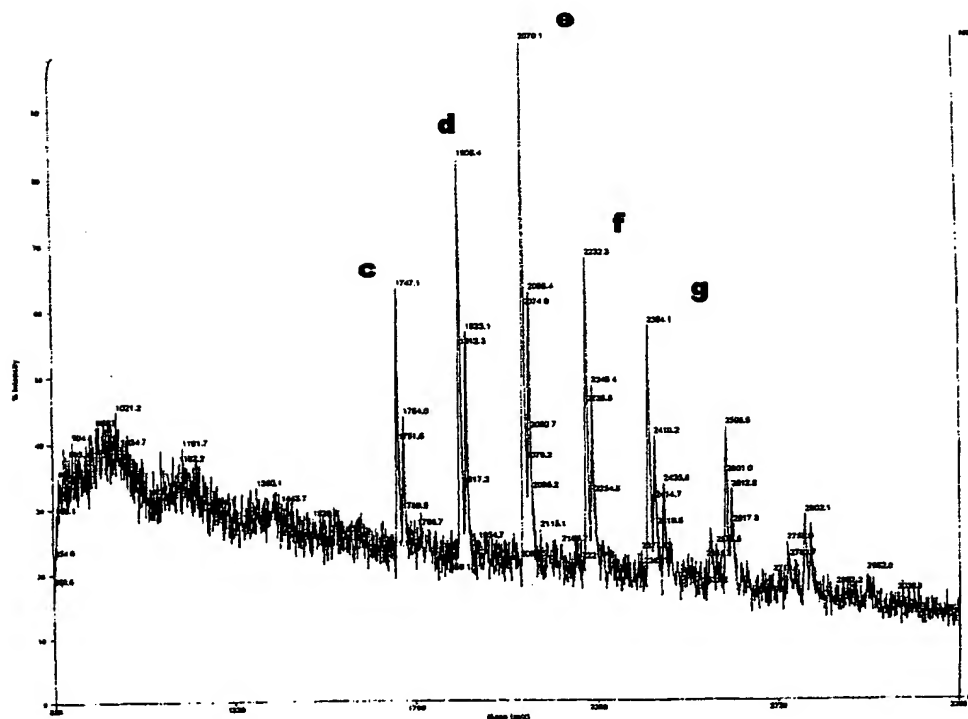
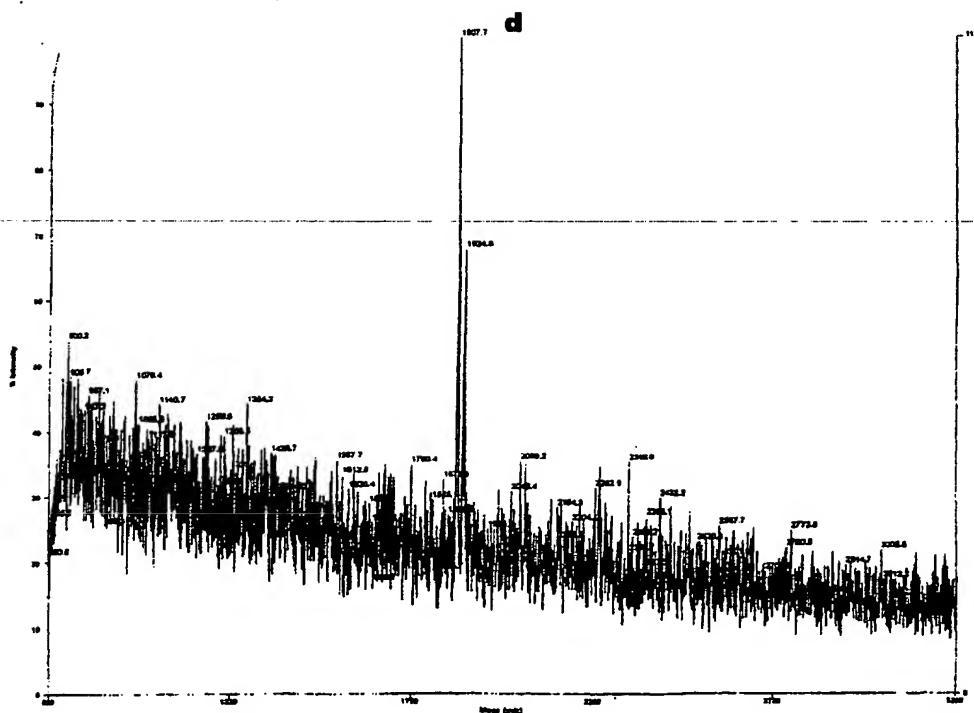


FIG. 11



A

FIG. 12



B

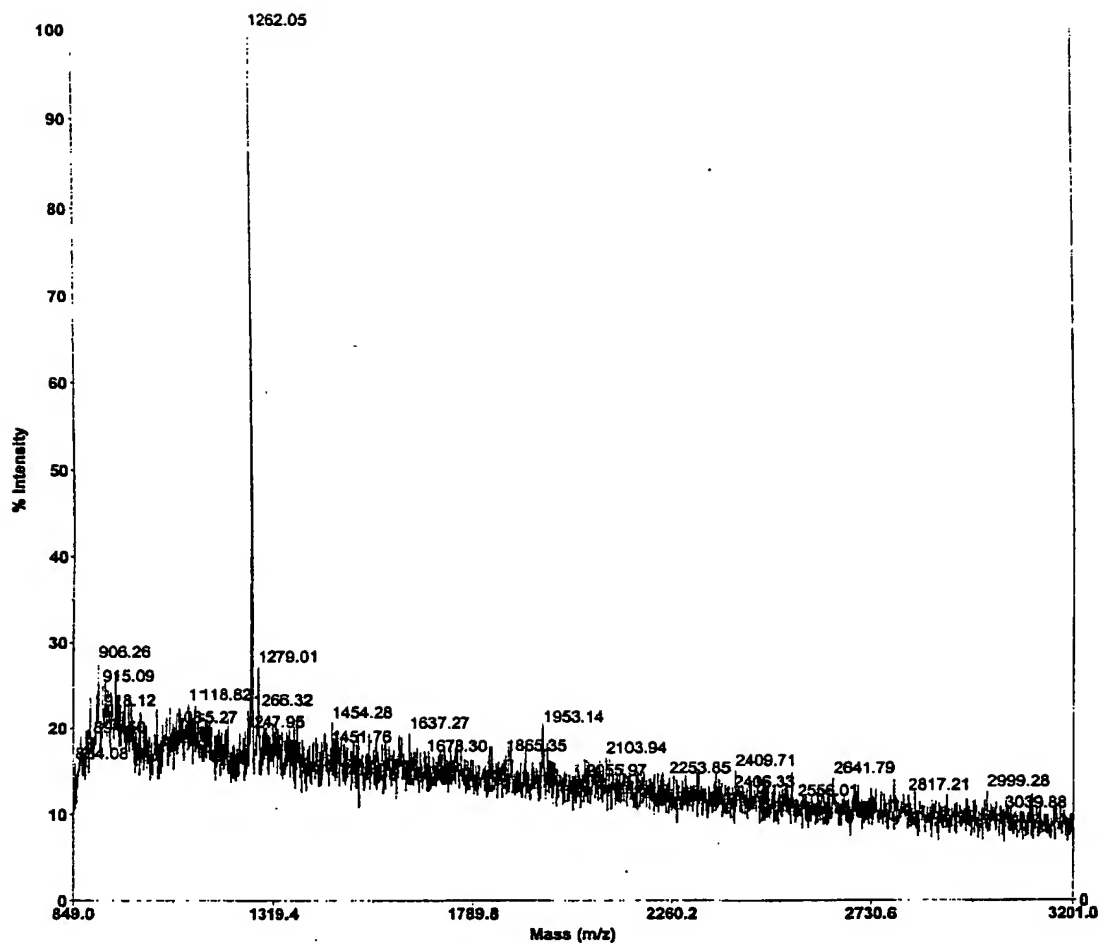


FIG. 12C

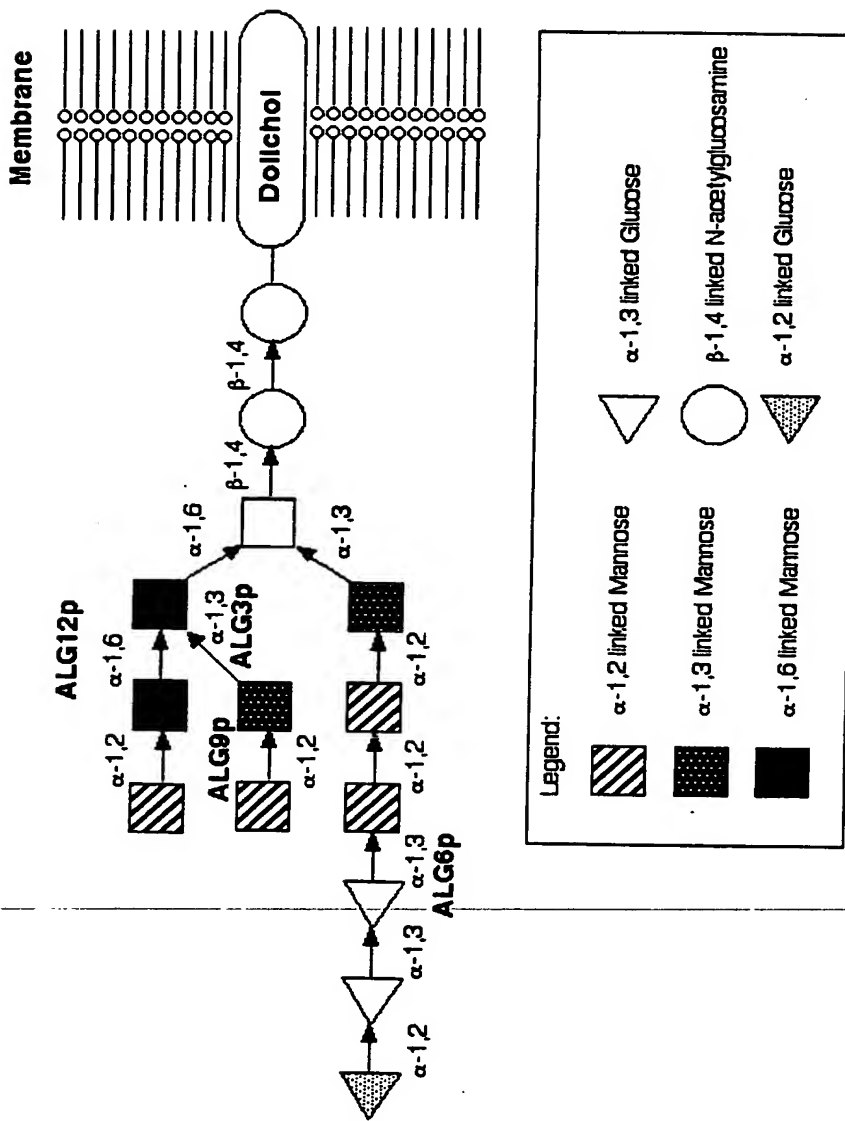


FIG. 13

**Lipid-linked N-glycans**

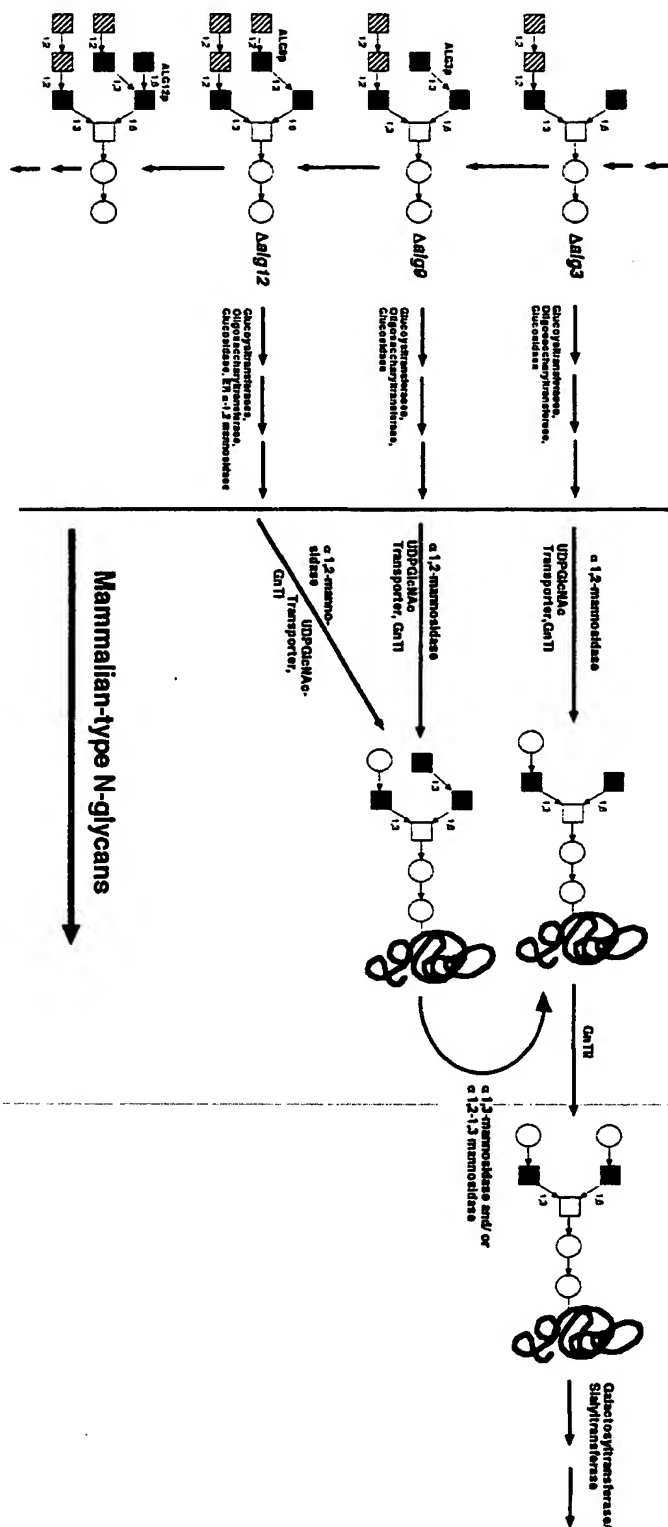


FIG. 14

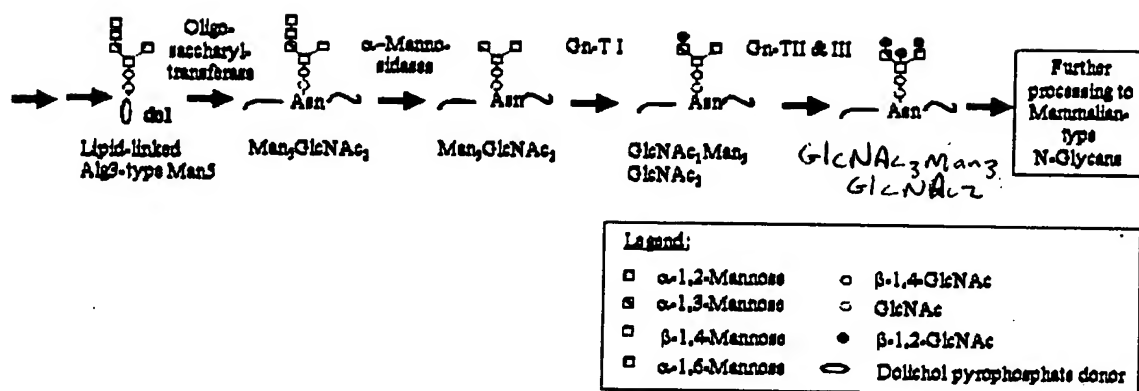


FIG. 15

## ALG3 Blast 05-22-01

Sequences producing significant alignments: (bits) Value

gi 586444 sp P38179 ALG3_YEAST	DOLICHYL-P-MAN:MAN(5)GLCNAC(...797	0.0
gi 3024226 sp Q92685 ALG3_HUMAN	DOLICHYL-P-MAN:MAN(5)GLCNAC...173	7e-43
gi 3024221 sp Q24332 NT56_DROVI	LETHAL(2)NEIGHBOUR OF TID P...145	3e-34
gi 3024222 sp Q27333 NT56_DROME	LETHAL(2)NEIGHBOUR OF TID P...121	3e-27
gi 10720153 sp P82149 NT53_DROME	LETHAL(2)NEIGHBOUR OF TID ...121	5e-27
gi 1707982 sp P40989 GLS2_YEAST	1,3-BETA-GLUCAN SYNTHASE CO... 32	2.8
gi 1346146 sp P38631 GLS1_YEAST	1,3-BETA-GLUCAN SYNTHASE CO... 31	6.6

### Alignments

#### Yeast

>gi|586444|sp|P38179|ALG3\_YEAST DOLICHYL-P-  
 MAN:MAN(5)GLCNAC(2)-PP-DOLICHYL MANNOSYLTRANSFERASE  
 (DOL-P-MAN DEPENDENT ALPHA(1-3)-MANNOSYLTRANSFERASE)  
 (HM-1 KILLER TOXIN RESISTANCE PROTEIN)  
 Length = 458

Score = 797 bits (2059), Expect = 0.0  
 Identities = 422/458 (92%), Positives = 422/458 (92%)

Query: 1	MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVYVIFDCRANLIVMPLLLILFESMLCKI	60
Sbjct: 1	MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVYVIFDCRANLIVMPLLLILFESMLCKI	60
Query: 61	I I K K V A Y T E I D Y K A Y M E Q I E M I Q L D G M L D Y S Q V S G G T G P L V P A G H V L I Y K M M Y W L T E G M	120
Sbjct: 61	I I K K V A Y T E I D Y K A Y M E Q I E M I Q L D G M L D Y S Q V S G G T G P L V P A G H V L I Y K M M Y W L T E G M	120
Query: 121	D H V E R G Q V F F R Y L Y L L T L A L Q M A C Y Y L L H L P P W C V V L A C L S K R L H S I Y V L R L F N D C F T T L	180
Sbjct: 121	D H V E R G Q V F F R Y L Y L L T L A L Q M A C Y Y L L H L P P W C V V L A C L S K R L H S I Y V L R L F N D C F T T L	180
Query: 181	F M V V T V L G A I V A S R C H Q R P K L K K S L A L V I S A T Y S M A V S I K M N A L L Y F P A M M I S L F I L N D A	240
Sbjct: 181	F M V V T V L G A I V A S R C H Q R P K L K K S L A L V I S A T Y S M A V S I K M N A L L Y F P A M M I S L F I L N D A	240
Query: 241	N V I L T L L D L V A M I A W Q V A V A V P F L R S F P Q Q Y L H C A F N F G R K F M Y Q W S I N W Q M M D E E A F N D	300
Sbjct: 241	N V I L T L L D L V A M I A W Q V A V A V P F L R S F P Q Q Y L H C A F N F G R K F M Y Q W S I N W Q M M D E E A F N D	300
Query: 301	K R F X X X X X X X X X X X X X X F V T R Y P R I L P D L W S S L C H P L R K N A V L N A N P A K T I P F V L I A S N	360
Sbjct: 301	K R F H L A L L I S H L I A L T T L F V T R Y P R I L P D L W S S L C H P L R K N A V L N A N P A K T I P F V L I A S N	360
Query: 361	F I G V L F S R S L H Y Q F L S W Y H W T L P I L I F W S G M P F F V G P I W Y V L H E W C W N S Y P P N S Q X X X X X	420
Sbjct: 361	F I G V L F S R S L H Y Q F L S W Y H W T L P I L I F W S G M P F F V G P I W Y V L H E W C W N S Y P P N S Q	420
Query: 421	X X X X X X X X X X X X X X S G S V A L A K S H L R T T S S M E K K L N	458
Sbjct: 421	L A L N T V L L L L L A L T Q L S G S V A L A K S H L R T T S S M E K K L N	458



## Human

>gi|3024226|sp|Q92685|ALG3\_HUMAN DOLICHYL-P-MAN:MAN(5)GLCNAC(2)-PP-DOLICHYL  
 MANNOSYLTRANSFERASE

(DOL-P-MAN DEPENDENT ALPHA(1-3)-MANNOSYLTRANSFERASE)

(NOT56-LIKE PROTEIN)

Length = 438

Score = 173 bits (439), Expect = 7e-43

Identities = 133/396 (33%), Positives = 195/396 (48%), Gaps = 28/396 (7%)

Query: 26 WQDLKDGVRVIFDCRANLIVMPLILFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLD 85  
 WQ+ R ++ + R L+V L L E + +I +VAYTEID+KAYM ++E + ++  
 Sbjct: 29 WQER----RLLREPRYTLLVAACLCLAEVGITFWVIHRVAYTEIDWKAYMAEVEGV-IN 83

Query: 86 GMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFRYLYLLTLALQMACY 145  
 G DY+Q+ G TGPLVYPAG V I+ +Y+ T + Q F LYL TL L Y  
 Sbjct: 84 GTYDYTQLQGDGTGPLVYPAGFVYIFMGLYYATSRGTDIRMAQNI FAVLYLATLLLVFLIY 143

Query: 146 Y-LLHLPWC-VVLACL SKRLHSIYVLRFLNDCFTTFLMVVTVLGAIVASRCHQRPKLKK 203  
 + +PP+ + C S R+HSI+VLRFLND + + +L + QR  
 Sbjct: 144 HQTKVPPFVFFFMCCASYRVHSIFVLRFLNDP-----VAMVLLFLSINLLLAQRWGWG- 197

Query: 204 SLALVISATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVAVPF 263  
 +S+AVS+KMN LL+ P ++ L L L + A + QV + +PF  
 Sbjct: 198 -----CCFFSLAVSVKMNVLFLFAPGLLFLLLTQFGFRGALPKLGICAGL--QVVLGLPF 249

Query: 264 LRSFPQQYLHCAFNFGRKFMYQWSINWQMDDEAFNDKRFXXXXXXXXXXXXXXXXXVTRY 323  
 L P YL +F+ GR+F++ W++NW+ + E F + F + R+  
 Sbjct: 250 LLENPSGYLSRSFDLGRQFLFHWTVNWRFLPEALFLHRAFLALLTAHLTLLLLFALCRW 309

Query: 324 PRILPDWSSLCHPLRKNVILNANPAKTIPFVLIASNFIGVLFPSRSLHYQFLSWYHWTLP 383  
 R + S L P ++ I L SNFIG+ FSRSLHYQF WY TLP  
 Sbjct: 310 HRTGESILSLLRDPSKRKVPPOPLTPNQIVSTLFTSNFIGICFSRSLHYQFYVWYFHTLP 369

Query: 384 ILIF-----WSGMPFFVGPVIWYVLHEWCWNSYPPNS 414  
 L++ W + + + E WN+YP S  
 Sbjct: 370 YLLWAMPARWLTHLLRLVLGLI--ELSWNTYPSTS 403

## Drosophila Vi

>gi|3024221|sp|Q24332|NT56\_DROVI LETHAL(2)NEIGHBOUR OF TID PROTEIN (NOT58)  
 Length = 526

Score = 145 bits (366), Expect = 3e-34

Identities = 103/273 (37%), Positives = 157/273 (56%), Gaps = 17/273 (6%)

Query: 33 VRYVIFDCRANLIVMPLILFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQ 92  
 ++Y+ F+ A IV L++L E+++ ++I++V YTEID+KAYM++ E L+G +YS  
 Sbjct: 34 IKYLA FEPAALPIVSVLIVLAEAVINV LVIQRPVTEIDWKAYMQECEGF-LNGTTNYSL 92

Query: 93 VSGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFRYLYLLTLALQMACYLLH-LP 151  
 + G TGPLVYPA V IY +Y+LT +V Q F +YLL + L + Y +P  
 Sbjct: 93 LRGDTGPLVYPAAFVYIYSGLYYLTGQGTNVR LAQYIFACIYLLQMCVLRLYTKSRKVP 152

Query: 152 PWCVVLA CL-SKRLHSIYVLRFLNDCFTTFLMVVTVLGAIVASRCHQRPKLKKS LALVIS 210  
 P+ +VL+ S R+HSIYVLRFLND L +L A + QR L S  
 Sbjct: 153 PYVLVLSAFTSYRIHSIYVLRFLNDPVAIL-----LLYAALNLF LDQRWTLG-----S 200

Query: 211 ATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVAVPFLRSFPQQ 270  
 YS+AV +KMN + A + LF L + V+ TL+ L Q+ + PFLR+ P +  
 Sbjct: 201 ICYSLAVGVKMN--ILLFAPALLLFYLANLGVLRTLVQLTICAVLQLFIGAPFLRTHPME 258



Query: 271 YLHCAFNFGRKFMYQWSINWQMMDEEAFNDKRF 303  
YL +F+ GR F ++W++N++ + +E F + F  
Sbjct: 259 YLRGSFDLGRIFEHKWTVNYRFLSKELFEQREF 291

Score = 53.3 bits (127), Expect = 1e-06  
Identities = 31/62 (50%), Positives = 41/62 (66%), Gaps = 6/62 (9%)

Query: 352 IPFVLIASNFIGVLFSSRLHYQFLSWYHWTLPIILIFWSGMPFFVGPIWYVLH--EWCWNS 409  
+PF L NFIGV +RSLHYQF WY +LP L+ WS P+ +G + +L E+CWN+  
Sbjct: 412 LPFFL--CNFIGVACARSRLHYQFYIWFHSLPYLV-WS-TPYSLGVRYLILGLIEYCWN 467

Query: 410 YP 411  
YP  
Sbjct: 468 YP 469

## Drosophila melanogaster

>gi|3024222|sp|Q27333|NT56\_DROME LETHAL(2)NEIGHBOUR OF TID PROTEIN (NOT56)  
(NOT45)

Length = 510

Score = 121 bits (305), Expect = 3e-27  
Identities = 96/272 (35%), Positives = 154/272 (56%), Gaps = 17/272 (6%)

Query: 34 RYVIFDCRANLIVMPLLLIFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQV 93  
+Y++ + A IV ++L E ++ ++I++V YTEID+ AYM++ E L+G +YS +  
Sbjct: 36 KYLLLEPAALPIVGLFVLLAELVINVVVIRVPTYTEIDWVAYMQECEGF-LNGTTNYSLL 94

Query: 94 SGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFFRYLYLLTLALQMACYLLH-LPP 152  
G TGPLVYPA V IY +Y++T +V Q F +YLL LAL + Y +PP  
Sbjct: 95 RGD TGPLVYPAAFVYIYSALYYVTSHTGNVRLAQYIFAGIYLLQLALVRLYKSRKVPP 154

Query: 153 WCVVLA CL-SKRLHSIYVLR LFNDCFTT LFMVVTVLGAIVASRCHQRPKLKKS LALVISA 211  
+ +VL+ S R+HSIYVLR LFNDCFTT LFMVVTVLGAIVASRCHQRPKLKKS LALVISA 211  
Sbjct: 155 YVLVLSAFTSYRIHSIYVLR LFNDCFTT LFMVVTVLGAIVASRCHQRPKLKKS LALVISA 211

Query: 212 TYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVAVPFLRSFPQQY 271  
+S+AV +KMN + A + LF L + ++ T+L L Q+ + PFL + P +Y  
Sbjct: 203 FFSLAVGVKMN--ILLFAPALLLFYLANLGLLRTILQLAVCGVIQLLLGAFFLLTHPVEY 260

Query: 272 LHCAFNFGRKFMYQWSINWQMMDEEAFNDKRF 303  
L +F+ GR F ++W++N++ + + F ++ F  
Sbjct: 261 LRGSFDLGRIFEHKWTVNYRFLSRDVFENRTF 292

Score = 49.4 bits (117), Expect = 2e-05  
Identities = 27/60 (45%), Positives = 35/60 (58%), Gaps = 2/60 (3%)

Query: 352 IPFVLIASNFIGVLFSSRLHYQFLSWYHWTLPIILIFWSGMPFFVGPIWYVLHEWCWNSYP 411  
+PF L N +GV SRSRLHYQF WY +LP L + + V + L E+CWN+YP  
Sbjct: 407 LPFFL--CNLVGVACSRSLHYQFYVWFHSLPYLAWSTPYSLGVRCLILGLIEYCWN 464

Matrix: BLOSUM62  
Gap Penalties: Existence: 11, Extension: 1  
Number of Hits to DB: 28883317  
Number of Sequences: 96469  
Number of extensions: 1107545  
Number of successful extensions: 2870  
Number of sequences better than 10.0: 16  
Number of HSP's better than 10.0 without gapping: 5  
Number of HSP's successfully gapped in prelim test: 11  
Number of HSP's that attempted gapping in prelim test: 2839  
Number of HSP's gapped (non-prelim): 23

length of query: 458  
length of database: 35,174,128  
effective HSP length: 45  
effective length of query: 413  
effective length of database: 30,833,023  
effective search space: 12734038499  
effective search space used: 12734038499  
T: 11  
A: 40  
X1: 15 ( 7.1 bits)  
X2: 38 (14.6 bits)  
X3: 64 (24.7 bits)  
S1: 40 (21.8 bits)  
S2: 67 (30.4 bits)

FIG.16-4



*S. cerevisiae* ALG3

ATGGAAGGTGAACAGTCTCCGCAAGGTGAAAAGTCTCTGCAAAGGAAGC  
AATTTGTCAGACCTCCGCTGGATCTGTGGCAGGATCTCAAGGACGGTGTG  
CGCTACGTGATCTTCGATTGTAGGGCCAATCTTATCGTTATGCCCCTTTTG  
ATTTTGTTCGAAAGCATGCTGTGCAAGATTATCATTAAAGAAGGTAGCTTAC  
ACAGAGATCGATTACAAGGCGTACATGGAGCAGATCGAGATGATTCAGCT  
CGATGGCATGCTGGACTACTCTCAGGTGAGTGGTGGAACGGGGCCCGCTGG  
TGTATCCAGCAGGCCACGTCTTGATCTACAAGATGATGTACTGGCTAACA  
GAGGGAATGGACCACGTTGAGCGCGGGCAAGTGTTTTTCAGATACTTGTA  
TCTCCTTACACTGGCGTTACAAATGGCGTGTTACTACCTTTTACATCTACC  
ACCGTGGTGTGTGGTCTTGGCGTGCCTCTCTAAAAGATTGCACTCTATTTA  
CGTGCTACGGTTATTCAATGATTGCTTCACTACTTTGTTTATGGTCGTCACG  
GTTTTGGGGGCTATCGTGGCCAGCAGGTGCCATCAGCGCCCCAAATTTAAA  
GAAGTCCCTTGCGCTGGTGATCTCCGCAACATACAGTATGGCTGTGAGCA  
TTAAGATGAATGCGCTGTTGTATTTCCCTGCAATGATGATTTCTCTATTCAT  
CCTTAATGACGCGAACGTAATCCTTACTTTGTTGGATCTCGTTGCGATGAT  
TGCATGGCAAGTCGCAGTTGCAGTGCCCTTCCTGCGCAGCTTTCCGCAACA  
GTACCTGCATTGCGCTTTTAATTTTCGGCAGGAAGTTTATGTACCAATGGAG  
TATCAATTGGCAAATGATGGATGAAGAGGCTTTCAATGATAAGAGGTTCC  
ACTTGCCCTTTTAATCAGCCACCTGATAGCGCTCACCACACTGTTTCGTCA  
CAAGATACCCTCGCATCCTGCCCCGATTTATGGTCTTCCCTGTGCCATCCGC  
TGAGGAAAAATGCAGTGCTCAATGCCAATCCCGCCAAGACTATTCCATTC  
GTTCTAATCGCATCCAACCTTCATCGGCGTCCTATTTTCAAGGTCCCTCCAC  
TACCAGTTTCTATCCTGGTATCACTGGACTTTGCCTATACTGATCTTTTGGT  
CGGGAATGCCCTTCTTCGTTGGTCCCATTGTTGACGTCTTGCACGAGTGGT  
GCTGGAATTCCTATCCACCAAACCTCACAAGCAAGCACGCTATTGTTGGCA  
TTGAATACTGTTCTGTTGCTTCTATTGGCCTTGACGCAGCTATCTGGTTCGG  
TCGCCCTCGCCAAAAGCCATCTTCGTACCACCAGCTCTATGGAAAAAAG  
CTCAACTGA

*S. cerevisiae* Alg3p

MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVYVIFDCRANLIVMPLLIL  
FESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGM LDYSQVSGGTGPLVYPAG  
HVLIIYKMMYWLTEGMDHVERGQVFFRYLYLLTLALQMACYLLHLPPWCV  
VLACLSKRLHSIYVLRLFNDCFTTFLMVVTVLGAIVASRCHQRPKLKSLALV  
ISATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVA  
VPFLRSFPQQYLHCAFNFGRKFMYQWSINWQMMDEEAFNDKRFHLALLISHL  
IALTTLVTRYPRILPDLWSSLCHPLRKNVNLNANPAKTIPFVLIASNFIGVLFS  
RSLHYQFLSWYHWTLPIIFWSGMPFFVGPIWYVLHEWCWNSYPPNSQASTL  
LLALNTVLLLLALTQLSGSVALAKSHLRTTSSMEKKLN

FIG. 17

*P. pastoris* ALG3

ATGCCTCCGATAGAGCCAGCTGAAAGGCCAAAGCTTACGCTGAAAAATGT  
TATCGGTGATCTAGTGGCTCTTATTCAAAACGTTTATTTAACCCAGATTTT  
AGTGTCTTCGTTGCACCTCTTTTATGGTTAGCTGATTCCATTGTTATCAAGG  
TGATCATTGGCACTGTTTCCTACACAGATATTGATTTTTCTTCATATATGCA  
ACAAATCTTTAAAATTTCGACAAGGAGAATTAGATTATAGCAACATATTTG  
GTGACACCGGTCCATTGGTTTACCCAGCCGGCCATGTTTCATGCTTACTCAG  
TACTTTCGTGGTACAGTGATGGTGGAGAAGACGTCAGTTTCGTTCAACAA  
GCATTTGGTTGGTTATACCTAGGTTGCTTGTTACTATCCATCAGCTCCTACT  
TTTTCTCTGGCTTAGGGAAAATACCTCCGGTTTATTTTGTTTTGTTGGTAGC  
GTCCAAGAGACTGCATTCAATATTTGTATTGAGACTCTTCAATGACTGTTT  
AACAAACATTTTTGATGTTGGCAACTATAATCATCCTTCAACAAGCAAGTAG  
CTGGAGGAAAGATGGCACAACCTATTCCATTATCTGTCCCTGATGCTGCAG  
ATACGTACAGTTTAGCCATCTCTGTAAAGATGAATGCGCTGCTATACCTCC  
CAGCATTCTACTACTCATATATCTCATTGTGACGAAAATTTGATTAAAG  
CCTTGGCACCTGTTCTAGTTTTGATATTGGTGCAAGTAGGAGTCGGTTATT  
CGTTCATTTTACCGTTGCACTATGATGATCAGGCAAATGAAATTCGTTCTG  
CCTACTTTAGACAGGCTTTTGAAGTTAGTCGCCAATTTCTTTATAAGTGGA  
CGGTTAATTGGCGCTTTTGAAGCAAGAACTTTCAACAATGTCCATTTTC  
ACCAGCTCCTGTTTGTCTCCATATTATTACGTTAGTCTTGTTTCATCCTCAA  
GTTCTCTCTCCTAAAAACATTGGAAAACCGCTTGGTAGATTTGTGTTGGA  
CATTTTCAAATTTTGAAGCCAACCTTATCTCCAACCAATATTATCAACGA  
CCCAGAAAGAAGCCCAGATTTTGTTTACACCGTCATGGCTACTACCAACTT  
AATAGGGGTGCTTTTTTGCAAGATCTTTACACTACCAGTTCCTAAGCTGGTA  
TGCGTTCTCTTTGCCATATCTCCTTTACAAGGCTCGTCTGAAGTTTATAGCA  
TCTATTATTGTTTATGCCGCTCACGAGTATTGCTGGTTGGTTTTCCAGCTA  
CAGAACAAAGTTCCGCGTTGTTGGTATCTATCTTACTACTTATCCTGATTC  
TCATTTTTACCAACGAACAGTTATTTCTTCTCAATCGGTCCCTGCAGAAA  
AAAAGAATACATAA

*P. pastoris* Alg3p

MPPIEPAERP KLT LKNVIGDLV ALIQNVLFNPDFS VFVAPLLWLADSIKVIIG  
TVSYTDIDESSYMQQIFKIRQGELDYSNIFGDTGPLVYPAGHVHAYSVLSWYS  
DGGEDVSFVQQA FGWLYLGCLLSISSYFFSGLGKIPPVYFVLLVASKRLHSIF  
VLR LFNDC LTTFLMLATIILQQASSWRKDGTIPLSVPDAADTYS LAISVKMN  
ALLYLPAFLLLIYLICDENLIKALAPVLVLILVQVGVGYSFILPLHYDDQANEIR  
SAYFRQAFDFSRQFLYKWTNVNWRFLSQETFNNVHFHQLLFALHIITLVLFILKF  
LSPKNIGKPLGRFVLDFKFWKPTLSPTNIINDPERSPDFVYTVMATTNLIGVLF  
ARSLHYQFLSWYAFSLPYLLYKARLNFIASIIVYAAHEYCWLVPATEQSSAL  
LVSILLILILIFTNEQLFPSQSVP AEKKNT

FIG. 18

# *P. pastoris* ALG3 BLAST

Sequences producing significant alignments: (bits) Value

qi 586444 sp P38179 ALG3 YEAST Dolichyl-P-Man:Man(5)GlcNAc(...	228	2e-58
qi 12802365 gb AAK07848.1 AF309689 10 putative NOT-56 manno...	212	8e-54
qi 984725 gb AAA75352.1  ORF 1	206	4e-52
qi 7492702 pir T39084 probable mannosyltransferase - fissi...	176	8e-43
qi 16226531 gb AAL16193.1 AF428424 1 At2g47760/F17A22.15 [A...	164	2e-39
qi 25367230 pir B84919 Not56-like protein [imported] - Ara...	164	3e-39
qi 25814791 emb CAB70171.2  Hypothetical protein K09E4.2 [C...	161	2e-38
qi 17535001 ref NP_496950.1  Putative plasma membrane membr...	160	3e-38
qi 1654000 emb CAA70220.1  Not56-like protein [Homo sapiens...	155	2e-36
qi 13279206 gb AAH04313.1 AAH04313 Unknown (protein for IMA...	154	2e-36
qi 22122365 ref NP_666051.1  hypothetical protein MGC36684 ...	150	3e-35
qi 21292031 gb EAA04176.1  agCP3388 [Anopheles gambiae str...	120	4e-26
qi 1780792 emb CAA71167.1  lethal(2)neighbour of tid [Droso...	114	3e-24

## Alignments

### *S. cerevisiae*

Score = 228 bits (580), Expect = 2e-58  
 Identities = 154/429 (35%), Positives = 229/429 (53%), Gaps = 37/429 (8%)

Query: 9 RPKLTLKNVIGDLVALIQNVLFNPDFS VFAPLLWLADSIKVIIGTVSYTDIDFSSYM 68  
 RP L L DL ++ V+F+ ++ V PLL L +S++ K+II V+YT+ID+ +YM  
 Sbjct: 20 RPPLDLWQ---DLKDGVRVIFDCRANLIVMPLLILFESMLCKIIKKVAYTEIDYKAYM 76

Query: 69 QQIFKIR-QGELDYSNIFGDTGPLVYPAGHVHAYSVLSWYSDGGEDVSFVQQAFGWLYLG 127  
 +QI I+ G LDYS + G TGPLVYPAGHV Y ++ W ++G + V Q F +LYL  
 Sbjct: 77 EQIEMIQLDGM LDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFFRYLYLL 136

Query: 128 CLLLSISSYFFSGLGKIPVYFVLLVASKRLHSIFVLRLFNDCLTTFMLLATI---IILQ 184  
 L L ++ Y+ L +PP VL SKRLHSI+VLRLFNDC TT M+ T+ I+  
 Sbjct: 137 TLALQMACYY--LLHLPPWCVVLA CLSKRLHSIYVLRLFNDCFTTLFMVTVLGAIVAS 193

Query: 185 QASSWRKDGTTIPLSVPAADTYSLAISVKMNXXXXXXXXXXXXXXXXXCDENLIKALAPXX 244  
 + K ++ L + + TYS+A+S+KMN D N+I L  
 Sbjct: 194 RCHQRPKLKKS LALVI---SATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLV 250

Query: 245 XXXXXXXXXXXXYSFILPLHYDDQANEIRSAYFRQAFDFSRQFLYKWTNVNWRFLSQETFNNV 304  
 F+ Y AF+F R+F+Y+W++NW+ + +E FN+  
 Sbjct: 251 AMIAWQVAVAVPFL-----RSFPQOYLHCAFNFGRKFMYQWSINWQMMDEEAFNDK-301

Query: 305 HFHQQLL FALHIITL-VLFILKFLSPKNIGKPLGRFVLDFKFWKPTLSPTNIIN-DPERS 362  
 FH L H+I L LF+ ++ R + D++ L ++N +P ++  
 Sbjct: 302 RFHLALLISHLIALTTLFVTRY-----PRILPDLWSSLCHPLRKNVLANPAKT 351

Query: 363 PDFVYTVMATTNLIGVLFARSLHYQFLSWYAFSLPYLLYKARLNFIASIIVYAAHEYCWL 422  
 F V+ +N IGVLF+RSLHYQFLSWY ++LP L++ + + F I Y HE+CW  
 Sbjct: 352 IPF---VLIASNFIGVLFARSRLHYQFLSWYHTLPILIFWSGMPFFVGPVIWYVLHEWCWN 408

Query: 423 VFPATEQSS 431  
 +P Q+S  
 Sbjct: 409 SYPPNSQAS 417



*Neurospora crassa*

Score = 212 bits (540), Expect = 8e-54  
Identities = 140/400 (35%), Positives = 212/400 (53%), Gaps = 29/400 (7%)

Query: 35 SVFVAPLLWLADSIKVIIGTVSYTDIDFSSYMQQIFKIRQGELDYSNIFGDTGPLVYP 94  
S + P L+L D+++ +II V YT+ID+++YM+Q+ +I GE DY+ + G TGPLVYP  
Sbjct: 33 SKLIPPALFLVDALLCGLIIWKVPYTEIDWAAAYMEQVSQILSGERDYTEKVRGGTGPLVYP 92

Query: 95 AGHVHAYSVLSWYSDGGEDVSFVQQAAGWLYLGCLLLSISSYFFSGLGKIPPVYFVLLVA 154  
A HV+ Y+ L +D G ++ QQ F LY+ L + + Y+ K PP F LL  
Sbjct: 93 AAHVYIYTGLYHLTDEGRNILLAQQLFAGLYMVT LAVVMGCYW---QAKAPPYLFPLLT 149

Query: 155 SKRLHSIFVLRNFNDCLTTFMLLATIIILQQASSWRKDGTTIPLSVPDAADTYSLAISVK 214  
SKRLHSIFVLR FNDC + I Q+ +W+ A Y+L + VK  
Sbjct: 150 SKRLHSIFVLRNFNDCAVLFLWLAIFFFQR-RNWQA-----GALLYTLGLGVK 197

Query: 215 MNXXXXXXXXXXXXXXXXXCDENLIKALAPXXXXXXXXXXXXXSFILPLHYDDQANEIRSAY 274  
M + + L F+ HY + Y  
Sbjct: 198 MTLTLLSLPAVGIVLFLGSG-SFVTTLQLVATMGLVQILIGVPFL--AHYPT-----Y 247

Query: 275 FRQAFDFSQFLYKWTNVNWRFLSQETFNNVHFHQLLFALHIITLVLFILKFLSPKNIGK 333  
+AF+ SRQF +KWTNVNWRF+ +E F + F L ALH++ L +FI +++ P K  
Sbjct: 248 LSRAFELSRQFFFKWTNVNWRFVGEIIFLSKGFALTLLALHVLVLGIFITTRWIKPAR--K 305

Query: 334 PLGRFVLIDIFKFWKPTLS-PTNIINDPERSPDFVYTMATTNLIGVLFARSLHYQFLSWY 392  
L + + + KP L+ P + + +P ++ T + + N +G+LFARSLHYQF ++  
Sbjct: 306 SLVQLISPVLLAGKPPLTVPEHRAARDVTPRYIMTTILSANAVGLLFARSLHYQFYAYV 365

Query: 393 AFSLPYLLYKARLNFIASIIIVYAAHEYCWLVPATEQSSA 432  
A+S P+LL++A L+ + +++A HE+ W VFP+T SSA  
Sbjct: 366 AWSTPFLLRAGLHPVLVYLLWAVHEWAWNVPSTPASSA 405

*Schizosaccharomyces pombe*

Score = 176 bits (445), Expect = 8e-43  
Identities = 132/390 (33%), Positives = 194/390 (49%), Gaps = 35/390 (8%)

Query: 42 LWLADSIKVIIGTVSYTDIDFSSYMQQIFKIRQGELDYSNIFGDTGPLVYPAGHVHAY 101  
L L + + II V YT+ID+ +YM+Q+ GE DY++ G TGPLVYP GHV Y  
Sbjct: 30 LLLLEIPFVFAIISKVPYTEIDWIAAYMEQVNSFLLGERDYKSLVGCTGPLVYPGGHVFLY 89

Query: 102 SVLSWYSDGGEDVSFVQQAAGWLYLGCLLLSISSYFFSGLGKIPPVYFVLLVASKRLHSI 161  
++L + +DGG ++ Q F ++Y + +I Y F + + P +VLL+ SKRLHSI  
Sbjct: 90 TLLYYLTDGGTNIVRAQYIFAFVYW--ITTAIVGYLFK-IVRAPFYIYVLLILSKRLHSI 146

Query: 162 FVLRNFNDCLTTFMLLATIIILQQASSWRKDGTTIPLSVPDAADTYSLAISVKMNXXXXX 221  
F+LRLFNDC + L + I+ W + A+ S+A SVKM+  
Sbjct: 147 FILRLFNDCGNS-LFSSLFILSSCKKKWVR-----ASILLSVACSVKMSSLLYV 194

Query: 222 XXXXXXXXXXXXCDENLIKALAPXXXXXXXXXXXXXSFILPLHYDDQANEIRSAYFRQAFDF 281  
L++ L P + + + +Y+ QAFDF  
Sbjct: 195 PAYLVL-----LLQILGPKKTWMHIFVIIIVQILFSIPF----LAYFWSYWTQAFDF 242

Query: 282 SRQFLYKWTNVNWRFLSQETFNNVHFHQLLFALHIITLVLFILKFLSPKNIGKPLGRFVLD 341  
R F YKWTNVNWRF+ + F + F + LH+ LV F K + + P  
Sbjct: 243 GRAFDYKWTNVNWRFI PRSIFESTSFSTSILFLHVALLVAFCTCKHWNKLSRATP----- 295

Query: 342 IFKFWKPTLSPTNIINDPERSPDFVYTMATTNLIGVLFARSLHYQFLSWYAFSLPYLLY 401  
F L+ + +P+F++T +AT+NLIG+L ARSLHYQF +W+A+ PYL Y

Sbjct: 296 -FAMVNSMLTLKPLPKLQLATPNFIFTALATSNLIGILCARSLHYQFYAWFAWYSPYLCY 354

Query: 402 KARLNFIASIIIVYAAHEYCWLVFPATEQSS 431  
+A I ++ EY W VFP+T+ SS

Sbjct: 355 QASFPAPIVIGLWMLQEYAWNVPSTKLSS 384  
*Arabidopsis thaliana*

Score = 164 bits (415), Expect = 2e-39  
Identities = 131/391 (33%), Positives = 194/391 (49%), Gaps = 29/391 (7%)

Query: 42 LWLADSIVIKVIIGTVSYTDIDFSSYMQQIFKIRQGELDYSNIFGDTGPLVYPAGHVHAY 101  
L LAD+I++ +II V YT ID+ +YM Q+ GE DY N+ GDTGPLVYPAG ++ Y

Sbjct: 39 LILADAILVALIIAYVPYTKIDWDAYMSQVSGFLGGERDYGNLKGDTGPLVYPAGFLYVY 98

Query: 102 SVLSWYSDGGEDVSFVQQAFGWLYLGCLLLSISSYFFSGLGKIPVYFVLLVASKRLHSI 161  
S + + G +V Q FG LY+ L + + Y + + +P LL SKR+HSI

Sbjct: 99 SAVQNLTGG--EVYPAQILFGVLYIVNLGIVLIIYVKTDV--VPWWALSLLCLSKRIHSI 154

Query: 162 FVLRLFNDCLTTFMLLATIIILQQASSWRKDGTTIPLSVPAADTYSLAISVKMNXXXXX 221  
FVLRLFNDC L+ A++ + +RK + + +S A+SVKMN

Sbjct: 155 FVLRLFNDCFAMTLLHASMALFL----YRKWHLGMLV-----FSGAVSVKMNVLLEYA 202

Query: 222 XXXXXXXXXXXCDENLIKALAPXXXXXXXXXXXXXYSFILPLHYDDQANEIRSAYFRQAFDF 281  
N+I ++ F++ +Y AFD

Sbjct: 203 PTLLELLKAM--NIIGVVSALAGAALAQILVGLPFLITYPV-----SYIANAFDL 251

Query: 282 SRQFLYKWTNVNRFLSQETFNNVHFHQLLFALHIITLVLFILKFLSPKNIGKPLGRFVLD 341  
R F++ W+VN++F+ + F + F L H+ LV F + K+ G +G

Sbjct: 252 GRVFIHFWSVNFKFVPERVFSKEFAVCLLIAHLFLLVAFA-NYKWCKHEGGIIGFMRSR 310

Query: 342 IFKFWKP-TLSPTNIINDPERSPDFVYTVMATTNLIGVLFARSLHYQFLSWYAFSLPYLL 400  
F P +LS +++ + + V T M N IG++FARSLHYQF SWY +SLPYLL

Sbjct: 311 HFFLTLPSSLSFSDVSASRIITKEHVVTAMFVGNFIGIVFARSLHYQFYSWYFSLPYLL 370

Query: 401 YKARLNFIASIIIVYAAHEYCWLVFPATEQSS 431

++ +I++ E CW V+P+T SS

Sbjct: 371 WRTPFPTWLRRLIMFLGIELCWNVPSTPSSS 401

FIG. 19-3





*K. lactis* ALG3

TTTGTTTACAAGCTGATACCAACGAACATGAATACACCGGCAGGTTTACT  
GAAGATTGGCAAAGCTAACCTTTTACATCCTTTTACCGATGCTGTATTCAG  
TGCGATGAGAGTAAACGCAGAACAAATTGCATACATTTTACTTGTTACCA  
ATTACATTGGAGTACTATTTGCTCGATCATTACACTACCAATTCCTATCTT  
GGTACCATTGGACGTTACCAGTACTATTGAATTGGGCCAATGTTCCGTATC  
CGCTATGTGTGCTATGGTACCTAACACATGAGTGGTGCTGGAACAGCTAT  
CCGCCAAACGCTACTGCATCCACACTGCTACACGCGTGTAACACATACTG  
TTATTGGCTGTATTCTTAAGAGGACCCGCAAACCTCGAAAAGTGGTGATAA  
CGAAACAACACACGAGAAAGCTGAG

*K. lactis* Alg3p

FVYKLIPTNMNTPAGLLKIGKANLLHPFTDAVFSAMRVNAEQIAYILLVTNYI  
GVLFARSLHYQFLSWYHWTLPVLLNWANVPYPLCVLWYLTHEWCWNSYPP  
NATASTLLHACNTYCYWLYSZEDPQTRKVVITKQHTRKL

FIG. 20

# *K. lactis* ALG3 BLAST

Score	E	(bits)	Value
Sequences producing significant alignments:			
qi 586444 sp P38179 ALG3_YEAST	Dolichyl-P-Man:Man(5)GlcNAc(...	125	1e-28
qi 984725 gb AAA75352.1	ORF 1	94	4e-19
qi 16226531 gb AAL16193.1 AF428424.1	At2g47760/F17A22.15 [A...	72	1e-12
qi 25367230 pir B84919	Not56-like protein [imported] - Ara...	72	1e-12
qi 21292031 gb EAA04176.1	agCP3388 [Anopheles gambiae str....	69	2e-11
qi 20892051 ref XP_148657.1	similar to Lethal(2)neighbour ...	65	2e-10

## Alignments

### *S. cerevisiae*

Score = 125 bits (314), Expect = 1e-28  
 Identities = 60/120 (50%), Positives = 83/120 (69%), Gaps = 1/120 (0%)  
 Frame = +3

Query: 66 ANLLHPFT-DAVFSAMRVNAEQIAYILLVTNYIGVLFARSLHYQFLSWYHWTLPVLLNWA 242  
 ++L HP +AV +A A+ I ++L+ +N+IGVLF+RSLHYQFLSWYHWTLP+L+ W+  
 Sbjct: 332 SSLCHPLRKNVAVLNANP--AKTIPFVLIASNFIGVLFSSRLHYQFLSWYHWTLPILIFWS 389

Query: 243 NVPYPLCVLWYLTHEWCWNSYPPNATASTLLHACNTYCYWLYS\*EDPQTRKVVITKQHTR 422  
 +P+ + +WY+ HEWCWNSYPPN+ ASTLL A NT L + + V + K H R  
 Sbjct: 390 GMPFFVGPVWYVLEWCWNSYPPNSQASTLLALNTVLLLLLA-LTQLSGSVALAKSHLR 448

### *A. thaliana*

Score = 72.0 bits (175), Expect = 1e-12  
 Identities = 42/107 (39%), Positives = 57/107 (53%), Gaps = 3/107 (2%)  
 Frame = +3

Query: 84 FTDVFSAMRVNAEQIAYILLVTNYIGVLFARSLHYQFLSWYHWTLPVLLNWANVPYPLC 263  
 F+D S + + E + + V N+IG++FARSLHYQF SWY ++LP LL P L  
 Sbjct: 322 FSDVSASRI-ITKEHVVTAMFVGNFIGIVFARSLHYQFYSWYFYSLPYLLWRTPFPTWLR 380

Query: 264 VLWYLTHEWCWNSYPPNATASTL---LHACNTYCYWLYS\*EDPQTRK 395  
 ++ +L E CWN YP ++S L LH WL DP K  
 Sbjct: 381 LIMFLGIELCWNVPSTPSSSGLLLCLHLIILVGLWLAPSVDPYQLK 427

FIG. 21

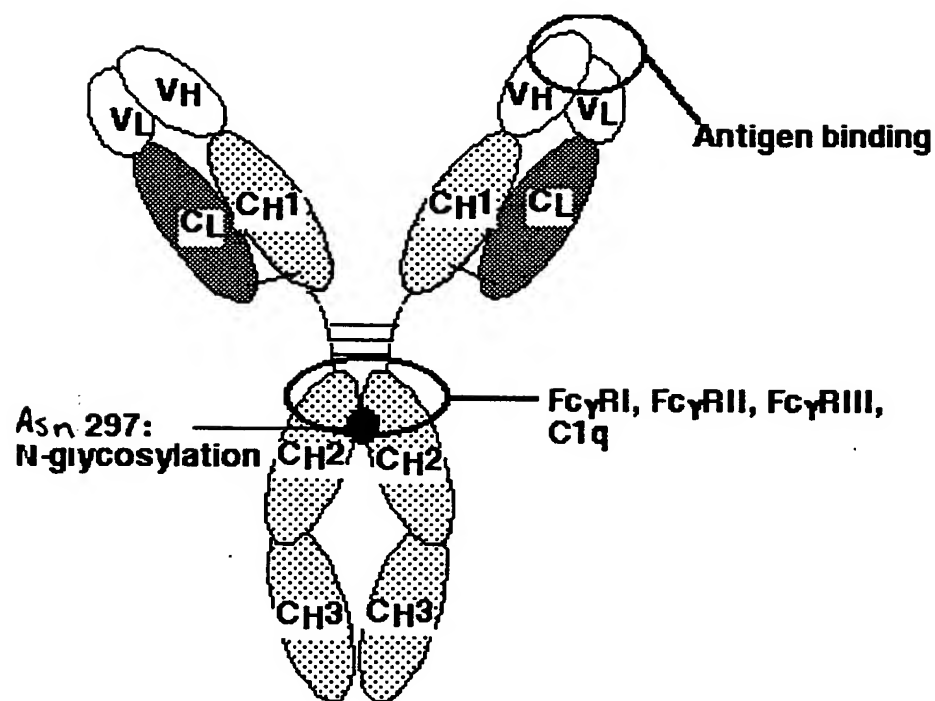


FIG. 22

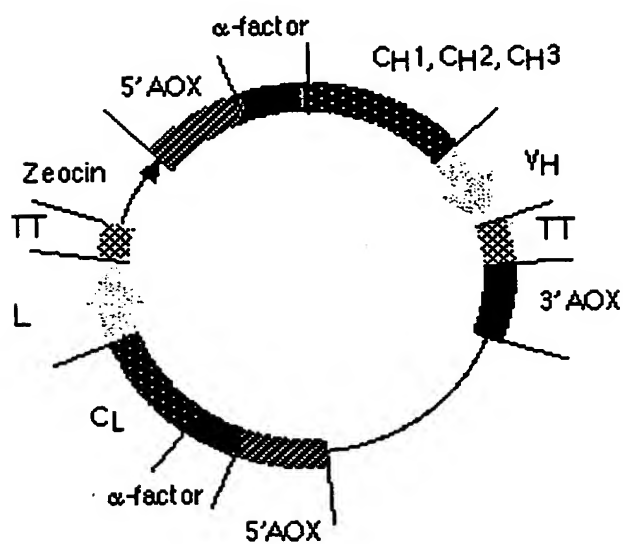


FIG. 23

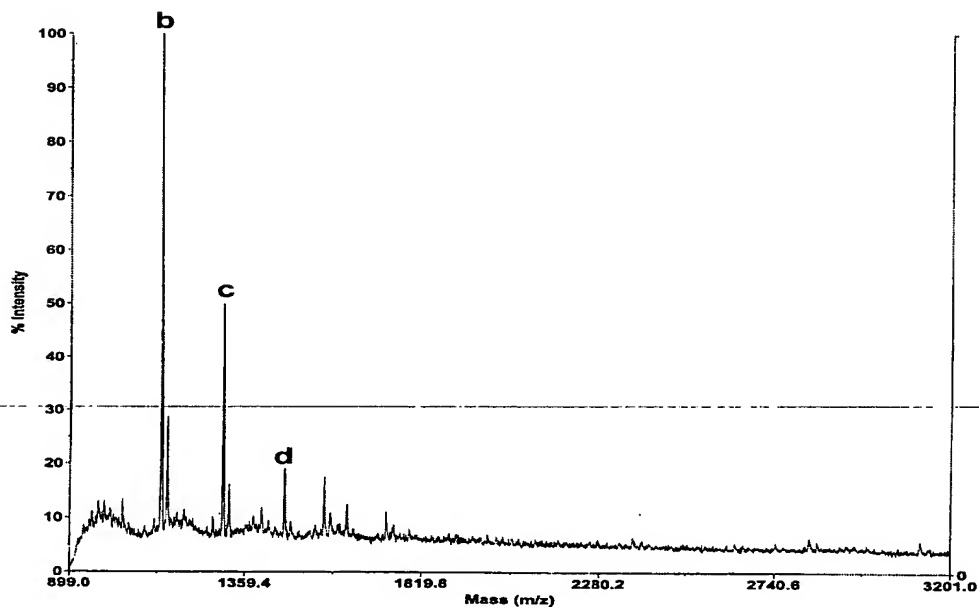
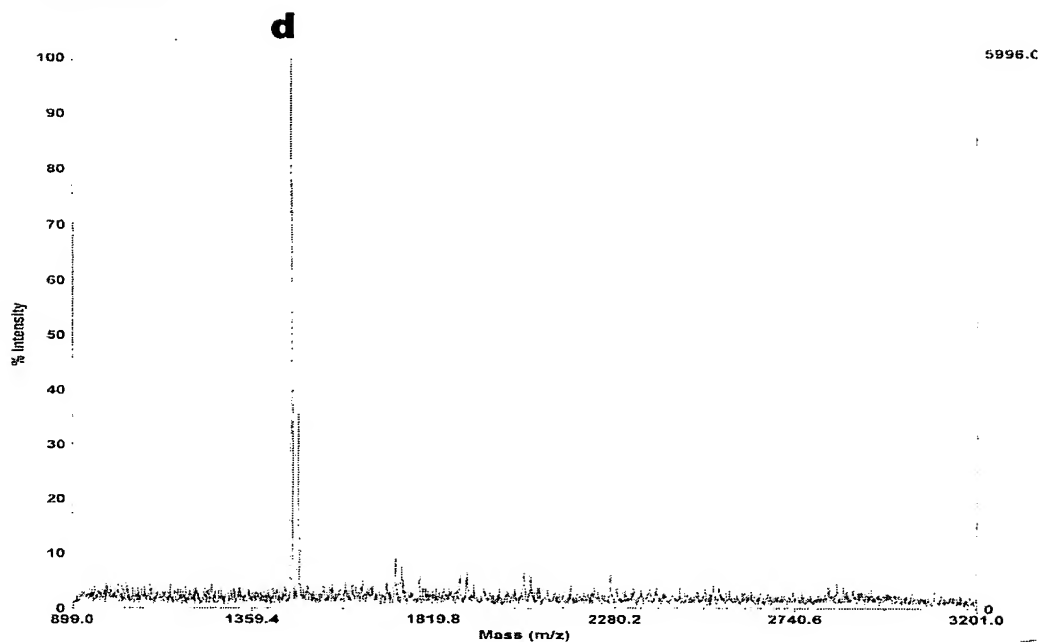
>gi|6754685|ref|NM\_010795.1| Mus musculus mannoside acetyl  
glucosaminyltransferase 3 (Mgat3), mRNA

ATGAAGATGAGACGCTACAAGCTCTTTCTCATGTTCTGTATGGCTGGCCTGTGCCTCATATCCTTCCTGC  
ACTTCTTTAAGACCTTATCCTATGTACCTTCCCAGAGAACTGGCCTCCCTCAGCCCTAACCTCGTATC  
CAGCTTCTTCTGGAACAATGCCCTGTCACTCCCAGGCCAGTCCGGAGCCGGGTGGCCCCGACCTATTG  
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CTGCTCAAGAACTATGACCAGTTCCGCTACTTGCTGGAAAATCCCTACCGGGAGCCCCAAGAGCACTGTAG  
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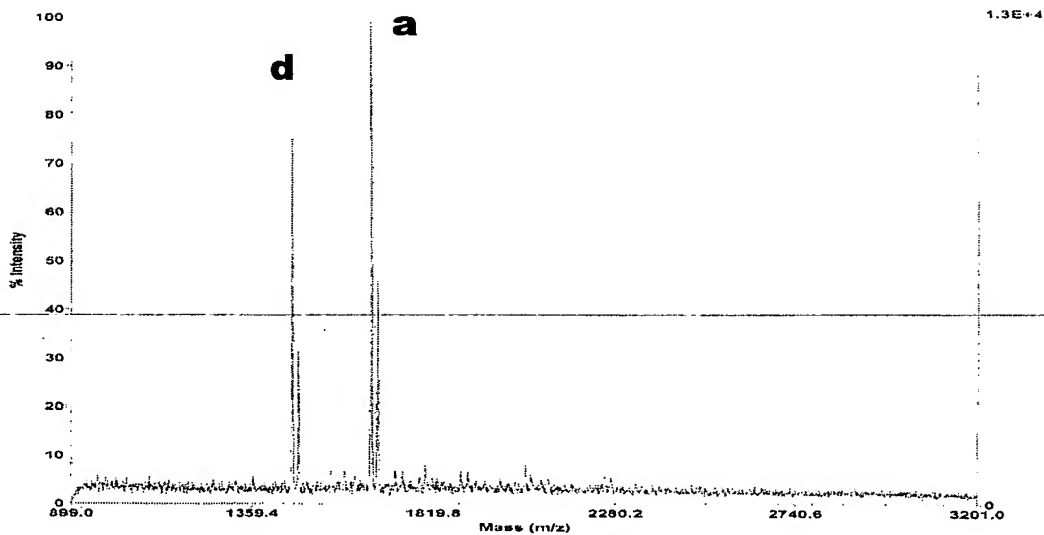
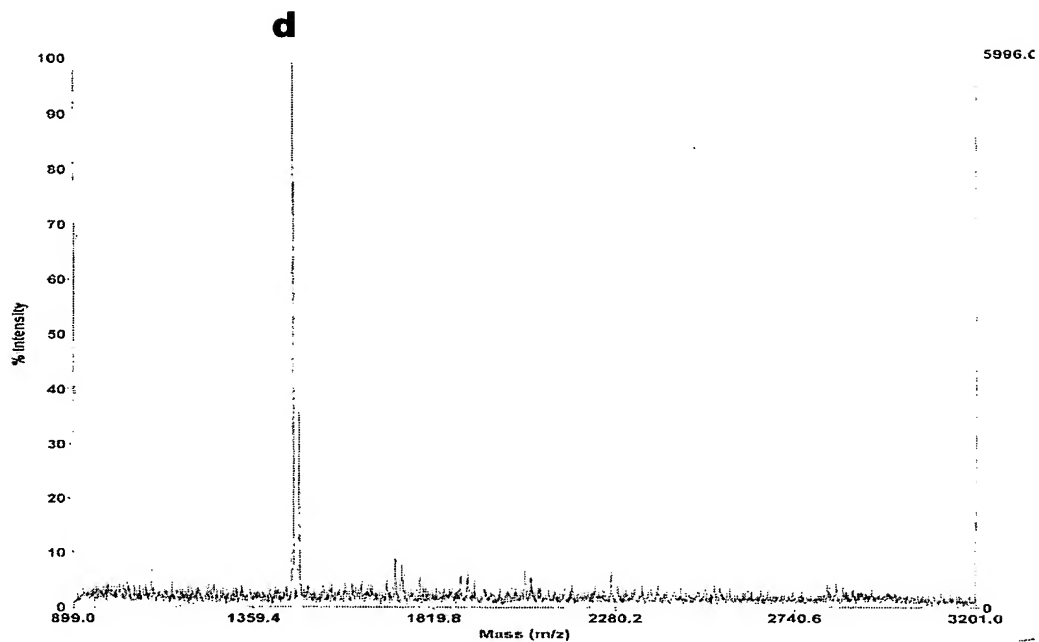
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acetylglucosaminyltransferase (EC 2.4.1.144) III - mouse  
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SSARGPARRPMRHLVSSRERLGSRGTRRKWVECVCLPGWHGSPSCGVPTVVQYSNLPKTERLVPREVP  
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YGF FWKQPGTLEVVSGCTMDMLQAVYGLDGIRLRRRQYYTMPNFRQYENRTGHILVQWSLGSPLHFAGWH  
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FIG. 24

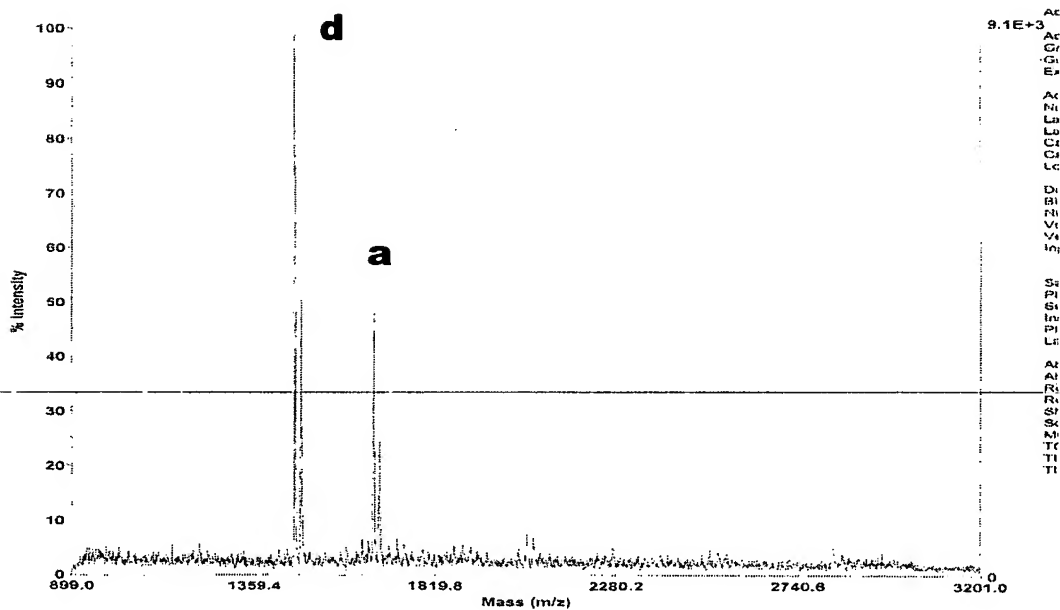
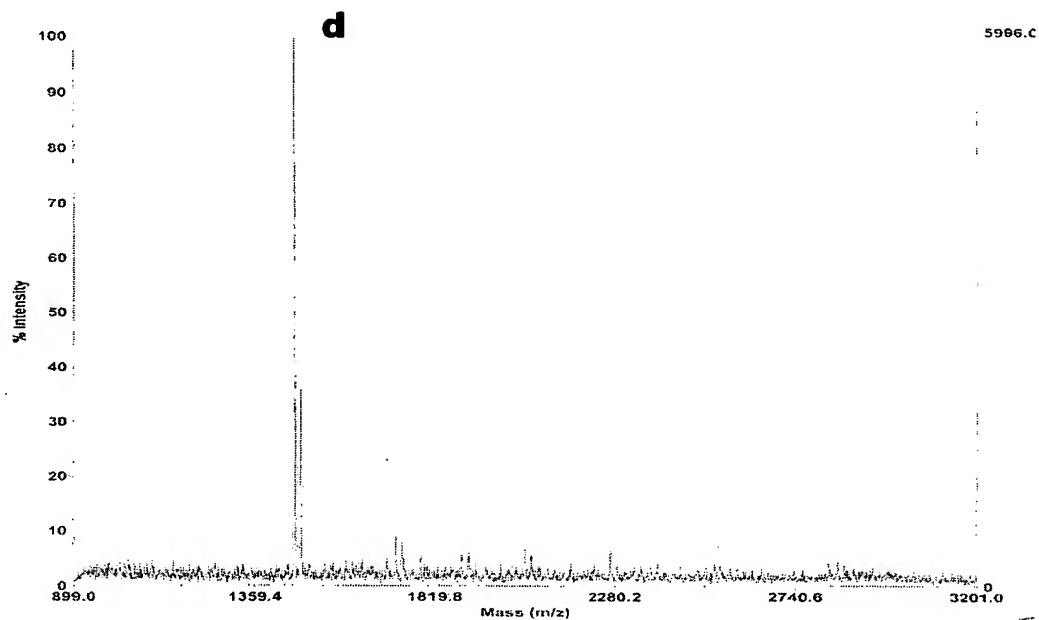
**Fig. 25**



**Fig. 26**

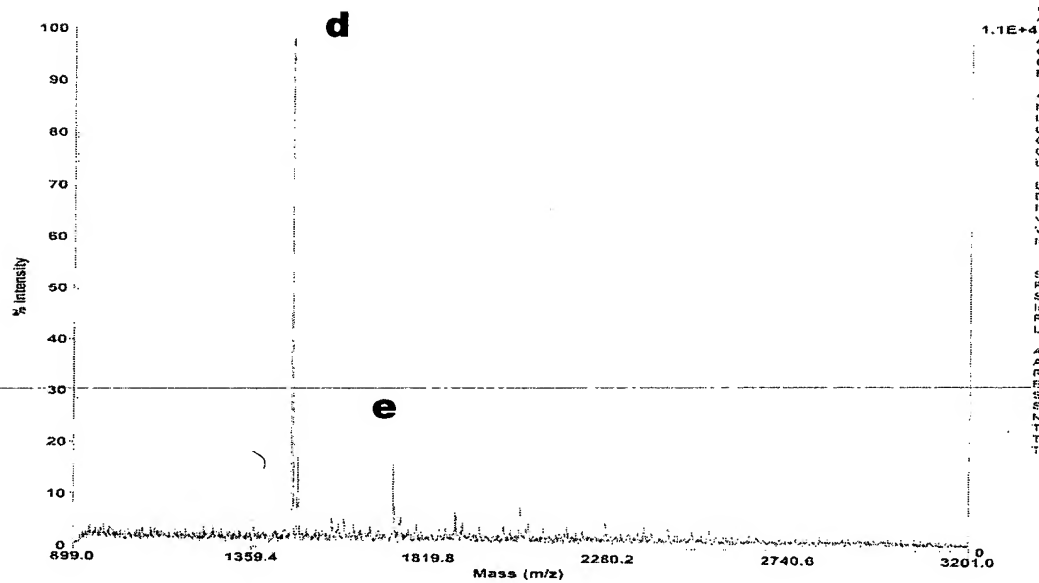
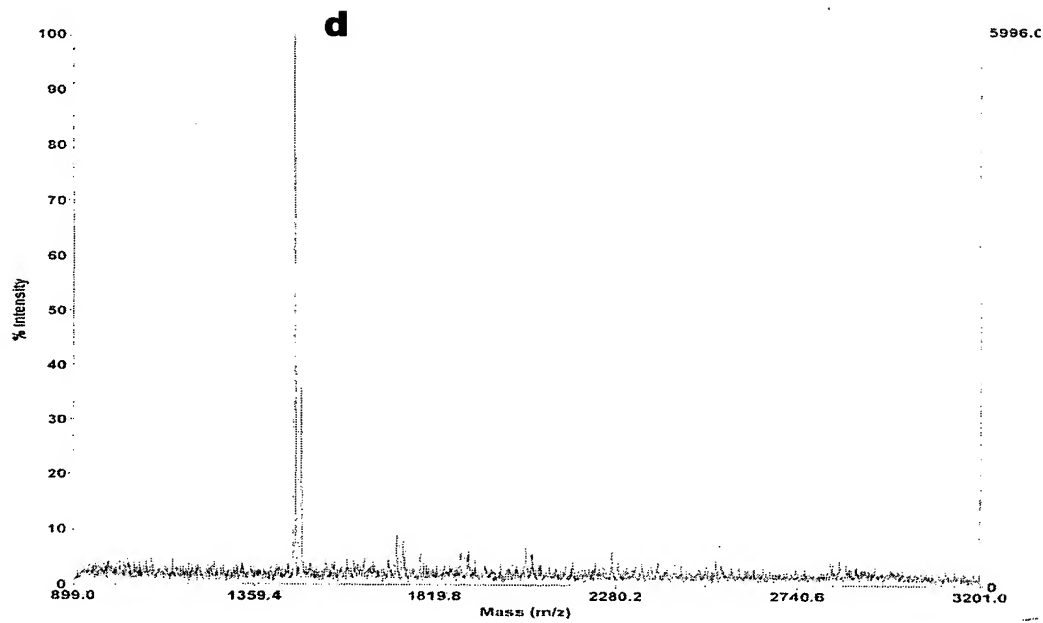


**Fig. 27**

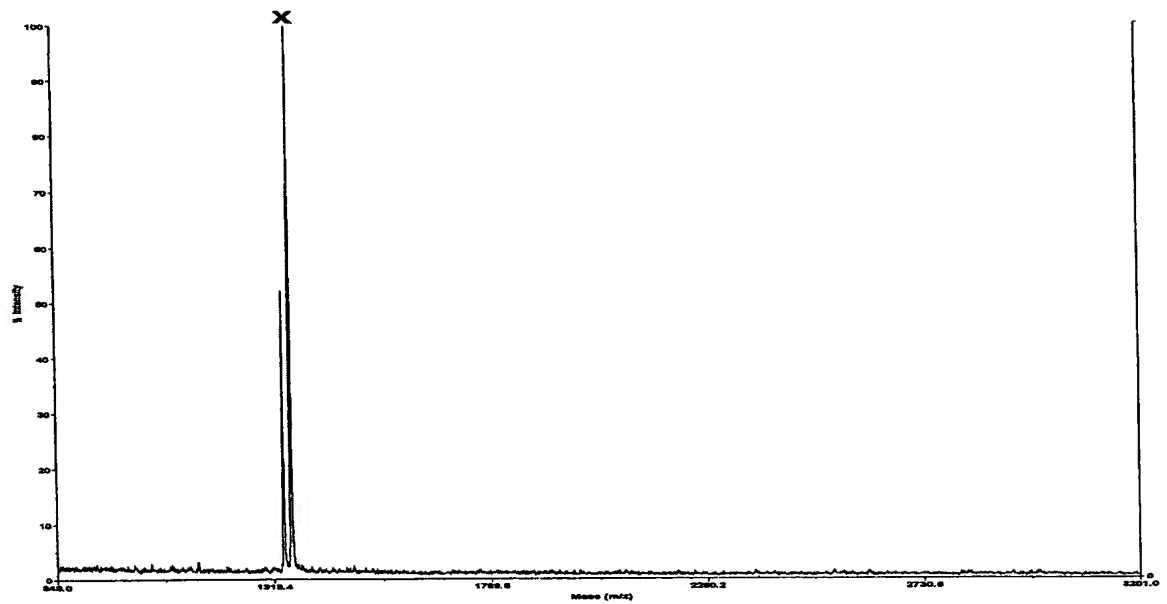




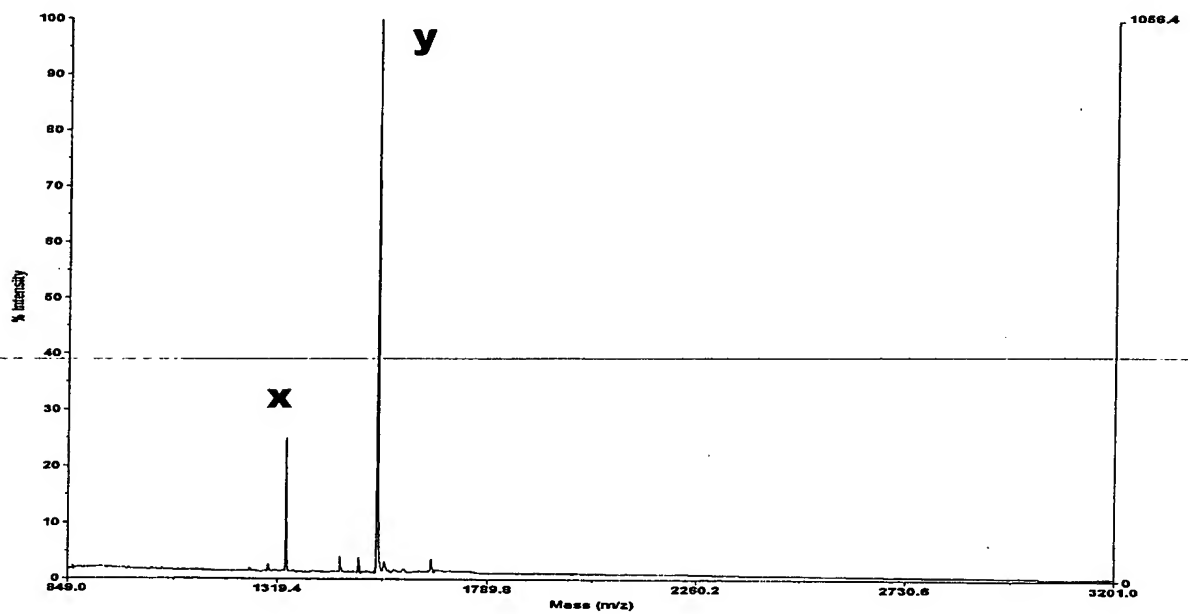
**Fig. 28**



**Fig. 29**

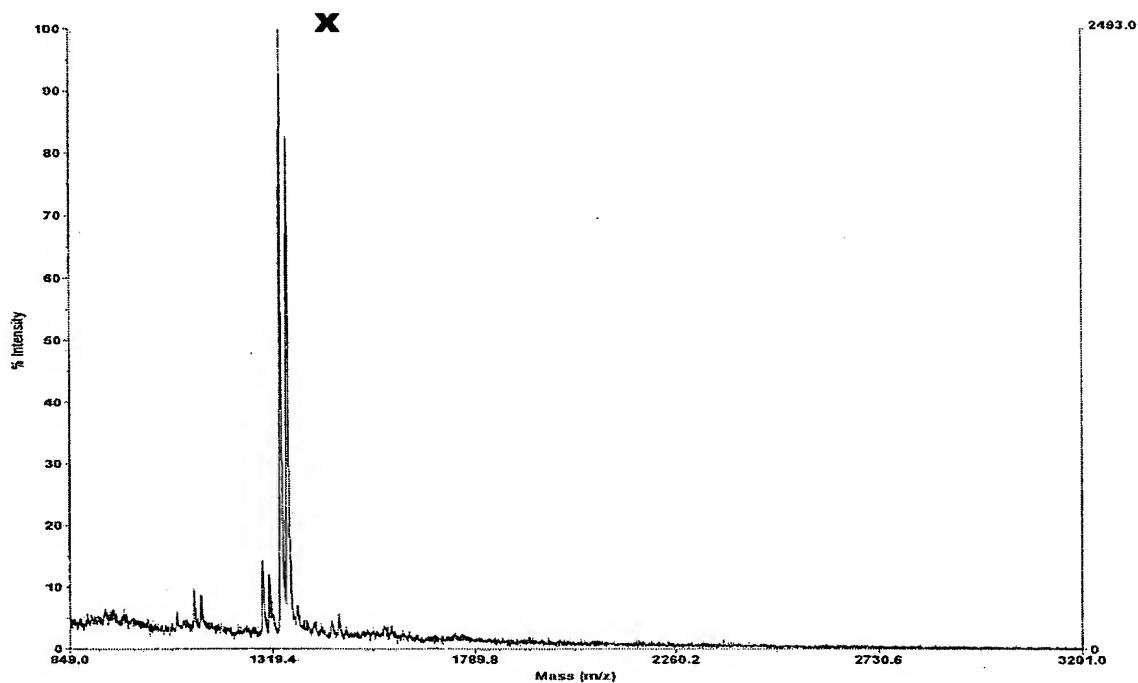


**Fig. 30**

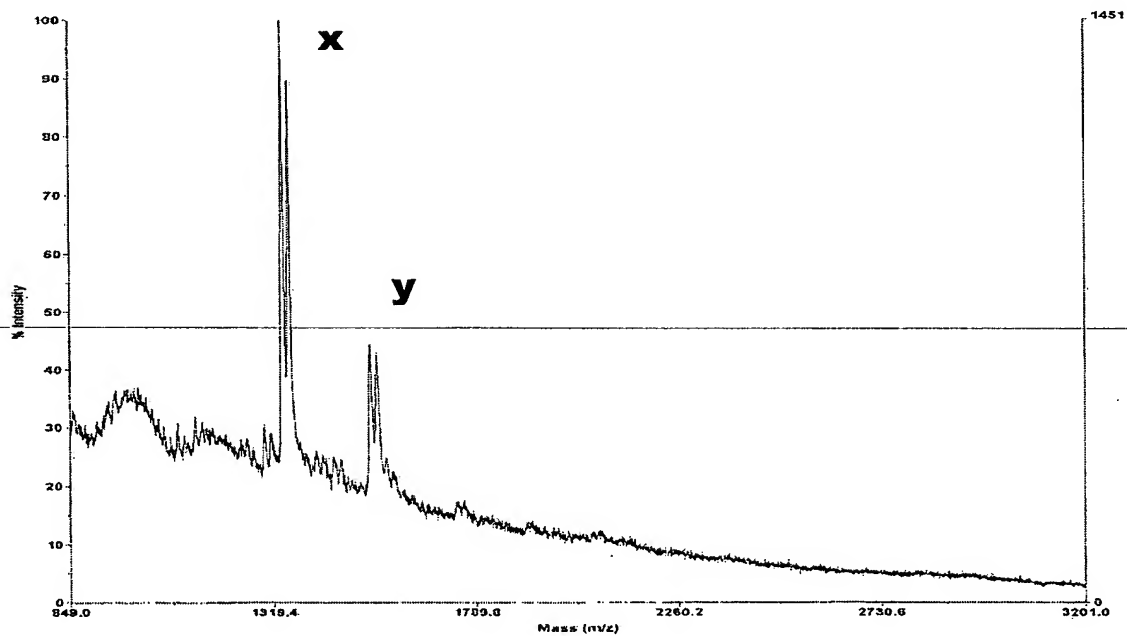


**Fig. 31**

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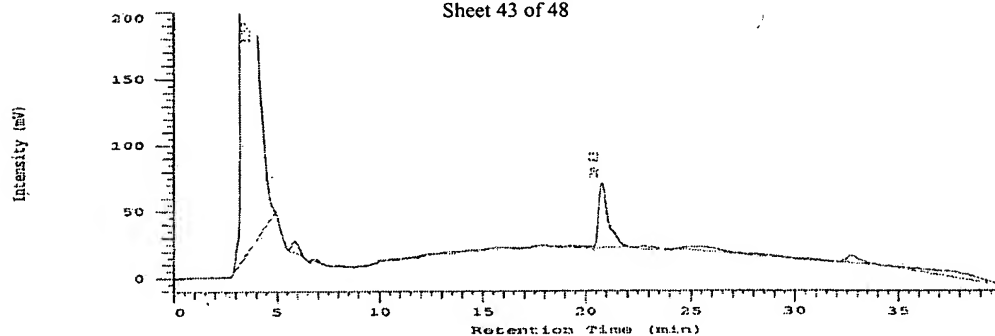
**Fig. 32**



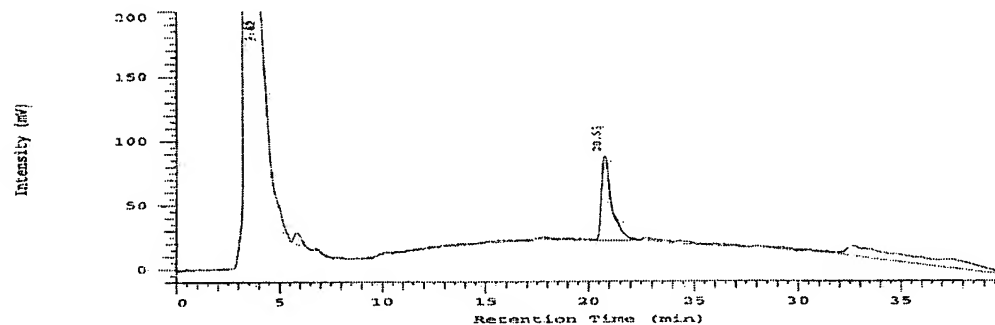
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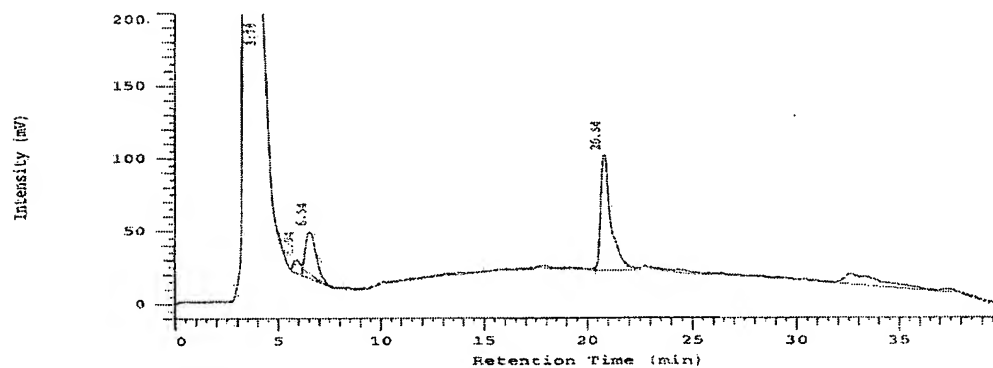
**A**



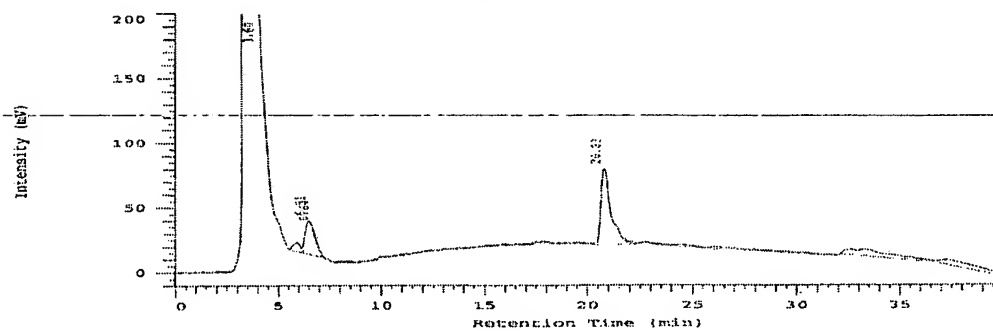
**B**



**C**



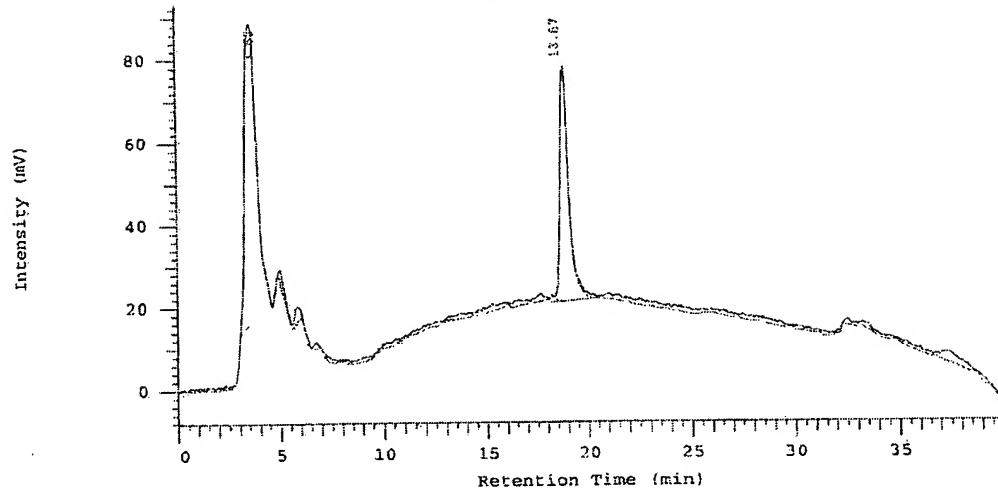
**D**



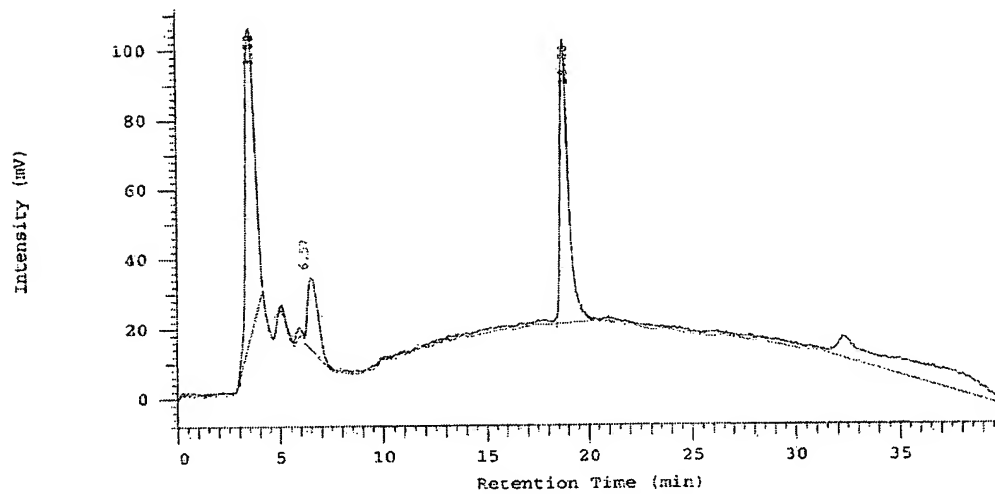
**Fig. 33**

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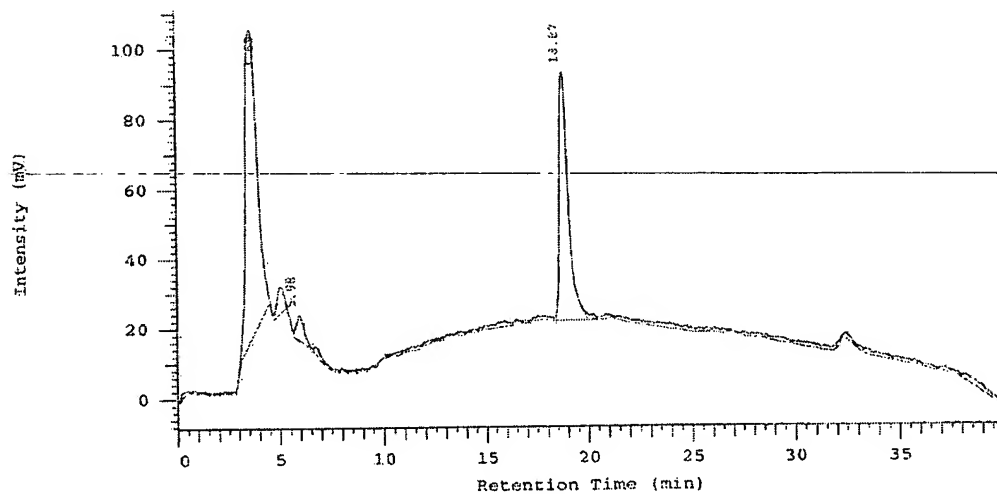
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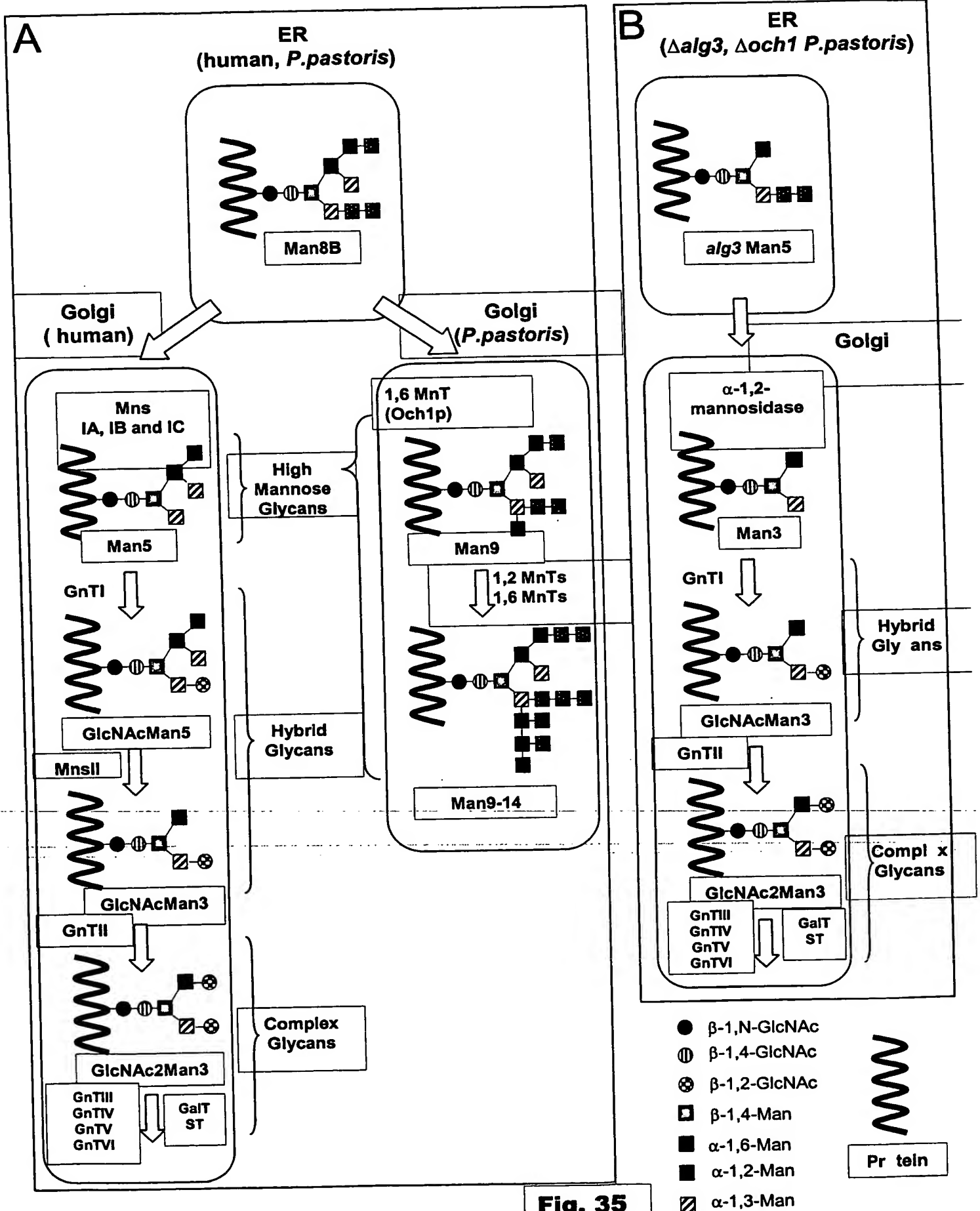
**B**



**C**



**Fig. 34**



**Fig. 36**

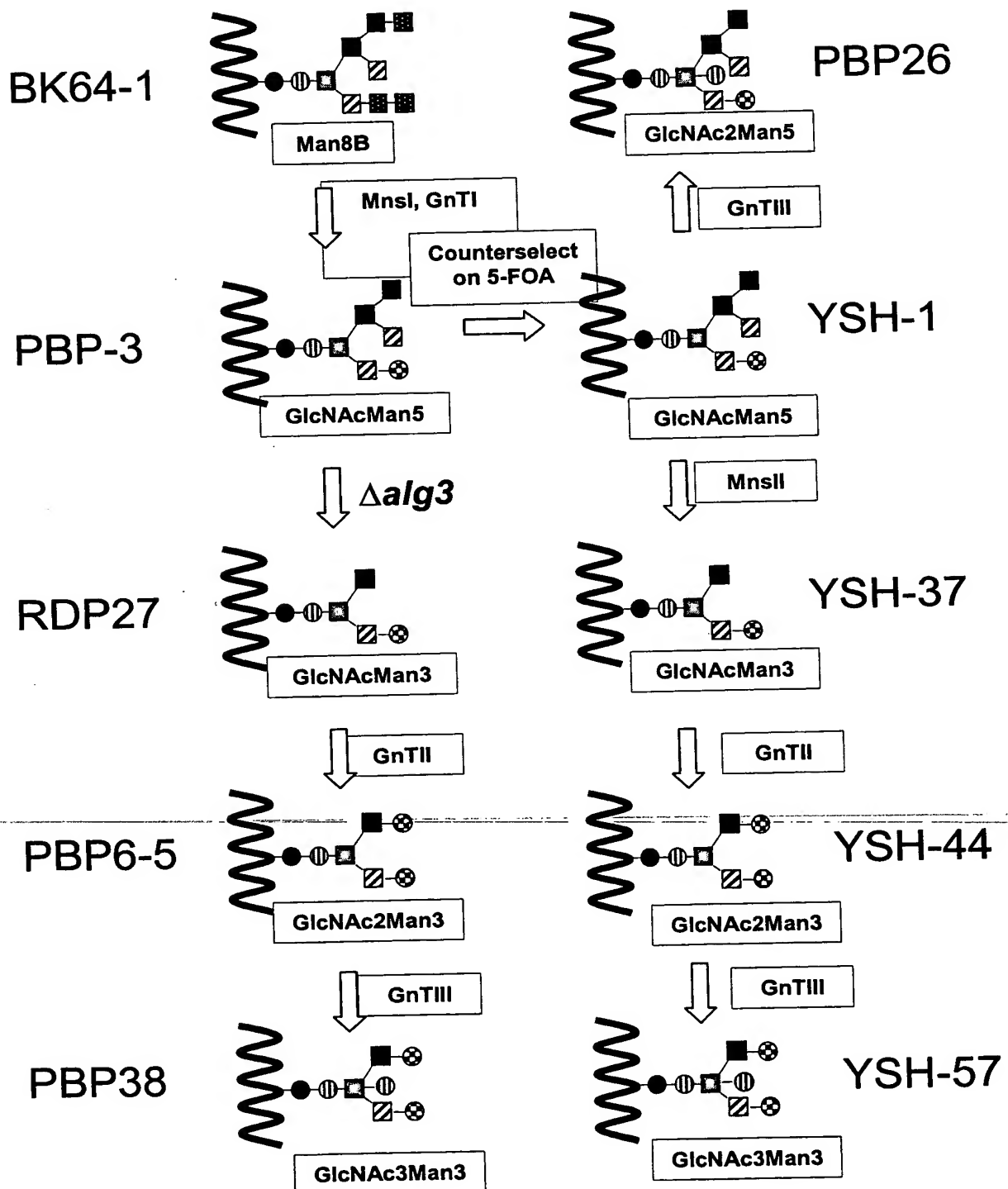


Diagram illustrating the enzymatic conversion of a branched oligosaccharide structure by the enzyme *GnT III*.

**Top Structure (Substrate):**

- Man  $\alpha$ 1,6
- Man  $\alpha$ 1,3
- Man  $\alpha$ 1,6
- Man  $\beta$ 1,4 - GlcNAc  $\beta$  1,4 - GlcNAc  $\beta$  1 - Asn
- GlcNAc  $\beta$ 1,2 - Man  $\alpha$ 1,3

**Enzyme:** *GnT III* (indicated by a downward arrow)

**Bottom Structure (Product):**

- Man  $\alpha$ 1,6
- Man  $\alpha$ 1,3
- Man  $\alpha$ 1,6
- GlcNAc  $\beta$ 1,4 — Man  $\beta$ 1,4 - GlcNAc  $\beta$  1,4 - GlcNAc  $\beta$  1 - Asn
- GlcNAc  $\beta$ 1,2 - Man  $\alpha$ 1,3

**Chemical Formulas:**

- Top:  $\text{GlcNAcMan}_5\text{GlcNAc}_2$
- Bottom:  $\text{GlcNAc}_2\text{Man}_5\text{GlcNAc}_2$



**Fig. 38**

